

Query Match 82.1%; Score 23; DB 11; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIH TA 28
|||||
Db 12 GKSIQDLRRRFFLHHLIAEIH TA 34

RESULT 14

US-10-372-095-23

; Sequence 23, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-095-23

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIH TA 28
|||||
Db 12 GKSIQDLRRRFFLHHLIAEIH TA 34

RESULT 15

US-10-340-484-2

; Sequence 2, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-2

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 16

US-10-340-484-3

; Sequence 3, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-340-484-3

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 17

US-10-340-484-4

```
; Sequence 4, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-340-484-4
```

```
Query Match          82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 GKSIQDLRRRFFLHHLIAEIHTA 28
          |||||
Db      12 GKSIQDLRRRFFLHHLIAEIHTA 34
```

RESULT 18

US-10-340-484-5

```
; Sequence 5, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-340-484-5

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHNTA 28
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 12 GKSIQDLRRRFFLHHLIAEIHNTA 34

RESULT 19

US-10-340-484-6
; Sequence 6, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-340-484-6

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHNTA 28
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 12 GKSIQDLRRRFFLHHLIAEIHNTA 34

RESULT 20

US-10-340-484-7
; Sequence 7, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.


```

; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Felis catus
US-10-340-484-7

```

```

Query Match          82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 GKSIQDLRRRFFLHHLIAEIHTA 28
        |||||
Db      12 GKSIQDLRRRFFLHHLIAEIHTA 34

```

```

RESULT 21
US-10-340-484-8
; Sequence 8, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Orycctolagus cuniculus
US-10-340-484-8

```

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 22

US-10-340-484-9

; Sequence 9, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-340-484-9

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 23

US-10-340-484-10

; Sequence 10, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215

; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-340-484-10

Query Match 82.1%; Score 23; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GKSIQDLRRRFFLHHLIAEIH TA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIH TA 34

RESULT 24

US-10-014-162-112

; Sequence 112, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-162-112

Query Match 82.1%; Score 23; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.8e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GKSIQDLRRRFFLHHLIAEIH TA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIH TA 34

RESULT 25

US-09-169-786-12

```
; Sequence 12, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-169-786-12
```

```
Query Match          82.1%;  Score 23;  DB 9;  Length 40;
Best Local Similarity 100.0%;  Pred. No. 8e-17;
Matches   23;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Qy          6 GKSIQDLRRRFFLHHLIAEIH TA 28
              |||||
Db          12 GKSIQDLRRRFFLHHLIAEIH TA 34
```

RESULT 26

US-09-843-221A-71

```
; Sequence 71, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTHrP
;   NAME/KEY: misc_feature
```

; LOCATION: (6)..(6)
; OTHER INFORMATION: D amino acid
US-09-843-221A-71

Query Match 78.6%; Score 22; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 7 KSIQDLRRRFFLHHLIAEIHTA 28

RESULT 27

US-09-843-221A-72

; Sequence 72, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified PTHrP
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: D amino acid
US-09-843-221A-72

Query Match 78.6%; Score 22; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 7 KSIQDLRRRFFLHHLIAEIHTA 28

RESULT 28

US-09-843-221A-75

```
; Sequence 75, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTHrP
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: D amino acid
US-09-843-221A-75
```

```
Query Match          78.6%; Score 22; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 KSIQDLRRRFFLHHLIAEIHTA 28
        |||||
Db      7 KSIQDLRRRFFLHHLIAEIHTA 28
```

RESULT 29

```
US-09-843-221A-67
; Sequence 67, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
```

```
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTHrP
US-09-843-221A-67
```

Query Match 78.6%; Score 22; DB 11; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.4e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KSIQDLRRRFFLHHLIAEIHTA 28
 | | | | | | | | | | | | | |
Db 12 KSIQDLRRRFFLHHLIAEIHTA 33

RESULT 30

US-09-843-221A-76

; Sequence 76, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

APPLICANT: LIU, CHUAN-FA

APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/214,860

PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

```

; SOFTWARE: PatentIn version 3.1

```

; SEQ ID NO 76

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-843-221A-76

Query Match 67.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.7e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      6  GKSIQDLRRRFFLHHLIAE  24
          |||||
Db     12  GKSIQDLRRRFFLHHLIAE  30

```

RESULT 31

US-09-843-221A-78

; Sequence 78, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 78
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: human PTHrP with non-human N-terminal peptide
 US-09-843-221A-78

Query Match 67.9%; Score 19; DB 11; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.9e-13;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAE 24
 |||||
 Db 13 GKSIQDLRRRFFLHHLIAE 31

RESULT 32

US-09-843-221A-79

; Sequence 79, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06


```

; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTHrP
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: D amino acid
US-09-843-221A-79

```

```

Query Match          64.3%;  Score 18;  DB 11;  Length 30;
Best Local Similarity 100.0%;  Pred. No. 9.4e-12;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      7 KSIQDLRRRFFLHHLIAE 24
        ||||||||||||||||
Db     13 KSIQDLRRRFFLHHLIAE 30

```

```

RESULT 33
US-09-843-221A-70
; Sequence 70, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified PTHrP
US-09-843-221A-70

```

```

Query Match          60.7%;  Score 17;  DB 11;  Length 28;

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Best Local Similarity 100.0%; Pred. No. 9.6e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRRFFLHHLIAEIHTA 28
 |||||
Db 12 LRRRFFLHHLIAEIHTA 28

RESULT 34

US-10-097-079-77

; Sequence 77, Application US/10097079

; Publication No. US20020132973A1

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.

; Morize, Isabelle

; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/097,079

; FILING DATE: 13-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/228,990

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 60/046,472

; FILING DATE: 14-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Martin Esq., Michael B.

; REGISTRATION NUMBER: 37,521

; REFERENCE/DOCKET NUMBER: A2678B-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-2793

; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: No. US20020132973A1 Relevant

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 12..16

; OTHER INFORMATION: /product= "OTHER"

; /note= "The side chains of Lys at position 12 and Asp at
; position 16 are linked by an amide bond."
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 28
; OTHER INFORMATION: /product= "OTHER"
; /note= "This C-terminal amino acid is an amide, i.e., CONH2."
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-097-079-77

Query Match 42.9%; Score 12; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 FLHHLIAEIHTA 28
| | | | | | | | | |
Db 17 FLHHLIAEIHTA 28

RESULT 35

US-10-097-079-71

; Sequence 71, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 71:

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: No. US20020132973A1 Relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: 18..22
;   OTHER INFORMATION: /product= "OTHER"
;   /note= "The side chains of Lys at position 18 and Asp at
;   position 22 are linked by an amide bond. "
; FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: 34
;   OTHER INFORMATION: /product= "OTHER"
;   /note= "This C-terminal amino acid is an amide, i.e., CONH2."
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-097-079-71

```

```

Query Match          42.9%; Score 12; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      17 FLHHLIAEIHTA 28
        |||||
Db      23 FLHHLIAEIHTA 34

```

```

RESULT 36
US-09-843-221A-77
; Sequence 77, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: modified human PTHrP
US-09-843-221A-77

Query Match 39.3%; Score 11; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRF 16
 |||||||
Db 12 GKSIQDLRRRF 22

RESULT 37

US-09-843-221A-150

; Sequence 150, Application US/09843221A
; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 150

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified human PTHrP

US-09-843-221A-150

Query Match 39.3%; Score 11; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGKSIQDLRRR 15
 |||||||
Db 11 LGKSIQDLRRR 21

RESULT 38

US-09-843-221A-114

; Sequence 114, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

```

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTHrP
US-09-843-221A-114

```

```

Query Match          39.3%; Score 11; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 LGKSIQDLRRR 15
        |||||
Db      11 LGKSIQDLRRR 21

```

```

RESULT 39
US-09-843-221A-65
; Sequence 65, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 36

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTHrP
US-09-843-221A-65

Query Match 39.3%; Score 11; DB 11; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRF 16
|||
Db 12 GKSIQDLRRRF 22

RESULT 40

US-09-843-221A-103
; Sequence 103, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTHrP
US-09-843-221A-103

Query Match 35.7%; Score 10; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRR 15
|||
Db 6 GKSIQDLRRR 15

Search completed: January 14, 2004, 11:15:11
Job time : 19.8411 secs

1	5	17.9	31	11	Q91Y90	Q91y90 peromyscus
2	5	17.9	31	11	Q91Y91	Q91y91 peromyscus
3	5	17.9	31	16	Q8KCG1	Q8kcg1 chlorobium
4	5	17.9	35	15	Q8JAC6	Q8jac6 human immun
5	5	17.9	39	2	Q51595	Q51595 pelobacter
6	4	14.3	28	10	Q8GZQ8	Q8gzq8 hordeum vul
7	4	14.3	28	12	Q67781	Q67781 human adeno
8	4	14.3	28	12	Q67780	Q67780 human adeno
9	4	14.3	29	2	Q9R4S6	Q9r4s6 treponema d
10	4	14.3	29	4	Q96PP3	Q96pp3 homo sapien
11	4	14.3	29	13	P82235	P82235 rana tempor
12	4	14.3	30	2	Q8KYE4	Q8kye4 bacillus an
13	4	14.3	30	2	Q9JMV3	Q9jmv3 escherichia
14	4	14.3	30	8	Q32617	Q32617 marchantia
15	4	14.3	31	5	Q8MXE8	Q8mx8 caenorhabdi
16	4	14.3	31	8	Q9MS77	Q9ms77 phacus acum
17	4	14.3	31	13	Q9DFI7	Q9dfi7 monopterus
18	4	14.3	31	13	Q9DEW2	Q9dew2 coturnix co
19	4	14.3	31	13	Q9DFH7	Q9dfh7 mastacembel
20	4	14.3	31	13	Q9DFI2	Q9dfi2 brachydanio
21	4	14.3	31	13	Q9DFH8	Q9dfh8 mastacembel
22	4	14.3	31	13	Q9DFI6	Q9dfi6 monopterus
23	4	14.3	31	13	Q9DFI1	Q9dfi1 brachydanio
24	4	14.3	31	13	Q9DEW1	Q9dew1 coturnix co
25	4	14.3	31	13	Q9DEW3	Q9dew3 coturnix co
26	4	14.3	31	13	Q90Z24	Q90z24 monopterus
27	4	14.3	31	16	Q8KEV8	Q8kev8 chlorobium
28	4	14.3	31	16	Q8KEV3	Q8kev3 chlorobium
29	4	14.3	32	4	Q96Q53	Q96q53 homo sapien
30	4	14.3	32	15	Q9DZ37	Q9dz37 human immun
31	4	14.3	33	4	Q9P1T8	Q9plt8 homo sapien
32	4	14.3	33	4	Q8N4J9	Q8n4j9 homo sapien
33	4	14.3	33	10	Q9AR83	Q9ar83 pinus pinas
34	4	14.3	33	16	Q9RI14	Q9ri14 yersinia pe
35	4	14.3	34	2	Q9R5U1	Q9r5u1 campylobact
36	4	14.3	34	2	Q9RCC0	Q9rcc0 yersinia ps
37	4	14.3	34	2	Q9RCD1	Q9rcd1 yersinia pe
38	4	14.3	34	6	Q95LA4	Q95la4 macaca mula
39	4	14.3	34	6	Q95LA6	Q95la6 sus scrofa
40	4	14.3	34	11	Q91ZX2	Q91zx2 cavia porce
41	4	14.3	34	11	Q91ZX3	Q91zx3 rattus norv
42	4	14.3	34	15	Q78053	Q78053 human immun
43	4	14.3	34	15	Q91366	Q91366 human immun
44	4	14.3	34	16	Q8CSH2	Q8csh2 staphylococ
45	4	14.3	35	15	Q8J9Q9	Q8j9q9 human immun
46	4	14.3	35	15	Q8JAB2	Q8jab2 human immun
47	4	14.3	35	15	Q8JAB8	Q8jab8 human immun
48	4	14.3	35	15	Q75981	Q75981 human immun
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50	4	14.3	35	15	Q70824	Q70824 human immun
51	4	14.3	35	15	Q8JAC5	Q8jac5 human immun
52	4	14.3	35	15	Q8JAA0	Q8jaa0 human immun
53	4	14.3	35	15	Q91400	Q91400 human immun
54	4	14.3	35	15	Q8J9N6	Q8j9n6 human immun
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57	4	14.3	35	15	Q8JAB6	Q8jab6 human immun

58	4	14.3	35	15	Q8J9Q2	Q8j9q2	human	immun
59	4	14.3	35	15	Q8J9Q8	Q8j9q8	human	immun
60	4	14.3	35	15	Q8J9R6	Q8j9r6	human	immun
61	4	14.3	35	15	Q8JA96	Q8ja96	human	immun
62	4	14.3	35	15	Q8J9Q0	Q8j9q0	human	immun
63	4	14.3	35	15	Q8JAB0	Q8jab0	human	immun
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65	4	14.3	35	15	Q8JAA5	Q8jaa5	human	immun
66	4	14.3	35	15	Q77133	Q77133	human	immun
67	4	14.3	35	15	Q8JAB5	Q8jab5	human	immun
68	4	14.3	35	15	Q8JA85	Q8ja85	human	immun
69	4	14.3	35	15	Q8JA92	Q8ja92	human	immun
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71	4	14.3	35	15	Q8JA83	Q8ja83	human	immun
72	4	14.3	35	15	O40587	O40587	human	immun
73	4	14.3	35	15	Q8J9P0	Q8j9p0	human	immun
74	4	14.3	35	15	Q8J9P8	Q8j9p8	human	immun
75	4	14.3	35	15	Q8J9Q6	Q8j9q6	human	immun
76	4	14.3	35	15	Q8JA91	Q8ja91	human	immun
77	4	14.3	35	15	Q8JA90	Q8ja90	human	immun
78	4	14.3	35	15	Q8JAB9	Q8jab9	human	immun
79	4	14.3	35	15	Q8JAA7	Q8jaa7	human	immun
80	4	14.3	35	15	Q8JA86	Q8ja86	human	immun
81	4	14.3	35	15	Q8J9R5	Q8j9r5	human	immun
82	4	14.3	35	15	Q8J9R0	Q8j9r0	human	immun
83	4	14.3	35	15	Q8JAA3	Q8jaa3	human	immun
84	4	14.3	35	15	Q8J9P4	Q8j9p4	human	immun
85	4	14.3	35	15	O91346	O91346	human	immun
86	4	14.3	35	15	Q8JAA6	Q8jaa6	human	immun
87	4	14.3	35	15	Q8JA82	Q8ja82	human	immun
88	4	14.3	35	15	Q8JAC2	Q8jac2	human	immun
89	4	14.3	35	15	Q8J9R1	Q8j9r1	human	immun
90	4	14.3	35	15	Q8JA88	Q8ja88	human	immun
91	4	14.3	35	15	Q8J9Q5	Q8j9q5	human	immun
92	4	14.3	35	15	Q8J9C6	Q8j9c6	human	immun
93	4	14.3	35	15	Q8JA94	Q8ja94	human	immun
94	4	14.3	35	15	Q8J9P9	Q8j9p9	human	immun
95	4	14.3	35	15	Q8JAC3	Q8jac3	human	immun
96	4	14.3	35	15	Q8JA97	Q8ja97	human	immun
97	4	14.3	35	15	Q75970	Q75970	human	immun
98	4	14.3	35	15	Q8JA95	Q8ja95	human	immun
99	4	14.3	35	15	Q8J9R3	Q8j9r3	human	immun
100	4	14.3	35	15	Q8JAA9	Q8jaa9	human	immun
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102	4	14.3	35	15	Q8JA89	Q8ja89	human	immun
103	4	14.3	35	15	Q8J9Q7	Q8j9q7	human	immun
104	4	14.3	35	15	Q8J9P3	Q8j9p3	human	immun
105	4	14.3	35	15	Q8JA93	Q8ja93	human	immun
106	4	14.3	35	15	Q8JAA2	Q8jaa2	human	immun
107	4	14.3	35	15	Q8J9P2	Q8j9p2	human	immun
108	4	14.3	35	15	Q8JAB7	Q8jab7	human	immun
109	4	14.3	35	15	Q8JAA8	Q8jaa8	human	immun
110	4	14.3	35	15	Q8J9N8	Q8j9n8	human	immun
111	4	14.3	35	15	Q8JA98	Q8ja98	human	immun
112	4	14.3	35	15	Q75990	Q75990	human	immun
113	4	14.3	35	15	Q75989	Q75989	human	immun
114	4	14.3	35	15	Q70833	Q70833	human	immun

115	4	14.3	35	15	Q8J9R2	Q8j9r2 human immun
116	4	14.3	35	15	Q8JAC0	Q8jac0 human immun
117	4	14.3	35	15	Q76253	Q76253 human immun
118	4	14.3	35	15	Q70798	Q70798 human immun
119	4	14.3	35	15	Q8JAA4	Q8jaa4 human immun
120	4	14.3	35	15	Q8J9P6	Q8j9p6 human immun
121	4	14.3	35	15	Q8JA46	Q8ja46 human immun
122	4	14.3	35	15	Q70300	Q70300 human immun
123	4	14.3	35	15	Q8J9Q3	Q8j9q3 human immun
124	4	14.3	35	15	Q8J9C7	Q8j9c7 human immun
125	4	14.3	35	15	Q8J9Q1	Q8j9q1 human immun
126	4	14.3	35	15	Q8J9N7	Q8j9n7 human immun
127	4	14.3	35	15	Q8JAC1	Q8jac1 human immun
128	4	14.3	35	15	Q8JAB4	Q8jab4 human immun
129	4	14.3	35	15	Q8J9R4	Q8j9r4 human immun
130	4	14.3	35	15	Q8J9P7	Q8j9p7 human immun
131	4	14.3	35	15	Q8JAB3	Q8jab3 human immun
132	4	14.3	35	15	Q77250	Q77250 human immun
133	4	14.3	35	15	Q75955	Q75955 human immun
134	4	14.3	35	15	Q8J9Q4	Q8j9q4 human immun
135	4	14.3	35	15	Q70776	Q70776 human immun
136	4	14.3	35	15	Q8J9P1	Q8j9p1 human immun
137	4	14.3	35	15	Q8J9N9	Q8j n immun
138	4	14.3	35	15	Q70827	Q70827 human immun
139	4	14.3	35	15	Q8JA99	Q8ja99 human immun
140	4	14.3	35	16	Q9PBV9	Q9pbv9 xylella fas
141	4	14.3	35	16	Q8EXR3	Q8exr3 leptospira
142	4	14.3	35	16	Q8EEP3	Q8eep3 shewanella
143	4	14.3	36	4	Q15530	Q15530 homo sapien
144	4	14.3	36	15	Q79434	Q79434 human immun
145	4	14.3	36	15	Q79419	Q79419 human immun
146	4	14.3	36	16	Q8EYJ2	Q8eyj2 leptospira
147	4	14.3	37	2	Q45107	Q45107 bacillus ce
148	4	14.3	37	8	Q8MDC2	Q8mdc2 larix gmeli
149	4	14.3	37	12	Q8AY5MX1150XZ	Q8ayz0 goose circo
150	4	14.3	37	15	Q40237	Q40237 human immun
151	4	14.3	37	16	Q8CLL0	Q8cll0 yersinia pe
152	4	14.3	38	2	Q9FCW4	Q9fcw4 escherichia
153	4	14.3	38	2	Q9XCW6	Q9xcw6 rhodobacter
154	4	14.3	38	2	P97145	P97145 escherichia
155	4	14.3	38	4	Q9BWQ4	Q9bwq4 homo sapien
156	4	14.3	38	16	Q8X3X9	Q8x3x9 escherichia
157	4	14.3	39	10	Q9FEY1	Q9fey1 heterocapsa
158	4	14.3	39	11	Q9QWJ4	Q9qwj4 mus musculu
159	4	14.3	39	12	Q04259	Q04259 influenza a
160	4	14.3	39	15	Q90SK8	Q90sk8 human immun
161	4	14.3	39	15	Q90SK7	Q90sk7 human immun
162	4	14.3	39	16	Q8EZ33	Q8ez33 leptospira
163	4	14.3	40	4	P78340	P78340 homo sapien
164	4	14.3	40	4	Q9H3B8	Q9h3b8 homo sapien
165	4	14.3	40	12	Q8V647	Q8v647 rabies viru
166	4	14.3	40	12	Q9WGB3	Q9wgb3 human herpe
167	3	10.7	28	2	Q9AH13	Q9ah13 lactococcus
168	3	10.7	28	2	Q47736	Q47736 enterococcu
169	3	10.7	28	2	Q9ZG30	Q9zg30 chlamydia t
170	3	10.7	28	2	Q49327	Q49327 mycoplasma
171	3	10.7	28	2	Q9R5E6	Q9r5e6 thermus aqu

172	3	10.7	28	2	Q9REI4	Q9rei4	acidiphiliu	
173	3	10.7	28	2	Q9R5G3	Q9r5g3	bacteroides	
174	3	10.7	28	2	Q9XB41	Q9xb41	escherichia	
175	3	10.7	28	2	Q9R4Z2	Q9r4z2	lactobacill	
176	3	10.7	28	2	Q9ZIZ8	Q9ziz8	borrelia bu	
177	3	10.7	28	3	Q9UT99	Q9ut99	schizosacch	
178	3	10.7	28	3	Q9URF2	Q9urf2	trametes ve	
179	3	10.7	28	4	Q9UEN1	Q9uen1	homo sapien	
180	3	10.7	28	4	O43804	O43804	homo sapien	
181	3	10.7	28	4	Q96RV7	Q96rv7	homo sapien	
182	3	10.7	28	4	Q16325	Q16325	homo sapien	
183	3	10.7	1043Y	75X	737	Lengt5095737	homo sapien	
184	3	10.7	28	4	Q96G80	Q96g80	homo sapien	
185	3	10.7	28	4	Q8IXD3	Q8ixd3	homo sapien	
186	3	10.7	28	5	Q9BJE1	Q9bje1	pauropus sp	
187	3	10.7	28	5	Q9BJE0	Q9bje0	pauropus sp	
188	3	10.7	28	5	Q9BJE3	Q9bje3	pauropus sp	
189	3	10.7	28	5	Q9GPK5	Q9gpk5	scutigerell	
190	3	10.7	28	5	Q95P93	Q95p93	mesobuthus	
191	3	10.7	28	5	Q9BM76	Q9bm76	giardia lam	
192	3	10.7	28	5	Q9BM74	Q9bm74	giardia lam	
193	3	10.7	28	5	Q9GPK6	Q9gpk6	scutigerell	
194	3	10.7	28	5	Q9BJE2	Q9bje2	pauropus sp	
195	000XE	3	10.7	28	5	Q9BM68	Q9bm68	glottidia p
196	3	10.7	28	5	Q9BM75	Q9bm75	giardia lam	
197	3	10.7	28	6	Q9TRM4	Q9trm4	bos taurus	
198	3	10.7	28	6	Q9XS67	Q9xs67	bos taurus	
199	3	10.7	28	6	Q8MJG7	Q8mjg7	sus scrofa	
200	3	10.7	28	6	Q9N264	Q9n264	bos taurus	
201	3	10.7	28	6	Q9TSY9	Q9tsy9	gorilla gor	
202	3	10.7	28	8	Q9T4F8	Q9t4f8	meleagris g	
203	3	10.7	28	8	Q37005	Q37005	oryza sativ	
204	3	10.7	28	8	Q9T7L2	Q9t7l2	meleagris g	
205	3	10.7	28	8	Q9TIE9	Q9tie9	centella er	
XX206	3	10.7	28	8	Q9TIE8	Q9tie8	centY	
207	3	10.7	28	8	Q9T4F7	Q9t4f7	meleagris g	
208	3	10.7	28	8	Q9TIE6	Q9tie6	centella hi	
209	3	10.7	28	8	Q9T7L1	Q9t7l1	meleagris g	
210	3	10.7	28	8	Q9TIE7	Q9tie7	centella tr	
211	3	10.7	28	10	Q8S6H4	Q8s6h4	oryza sativ	
212	3	10.7	28	10	Q944P1	Q944p1	manihot esc	
213	3	10.7	28	11	Q99PL9	Q99pl9	mus musculu	
214	3	10.7	28	11	Q9QWC0	Q9qwc0	rattus sp.	
215	3	10.7	28	11	Q9QWQ3	Q9qww3	rattus norv	
216	3	10.7	28	11	P70542	P70542	rattus norv	
217	3	10.7	28	11	P97914	P97914	rattus norv	
218	3	10.7	28	11	Q62677			
219	3	10.7	28	11	O55021	O55021	mus musculu	
220	3	10.7	28	11	Q63743	Q63743	rattus norv	
221	3	10.7	28	11	Q8CFB9	Q8cfb9	mus musculu	
222	3	10.7	28	11	Q8C1H5	Q8clh5	mus musculu	
223	3	10.7	28	12	Q9WNI9	Q9wni9	tt virus. o	
224	3	10.7	28	12	Q68552	Q68552	hepatitis c	
225	3	10.7	28	13	Q9DD70	Q9dd70	gallus gall	
226	3	10.7	28	13	Q8QGY7	Q8qgy7	fugu rubrip	
227	3	10.7	28	13	O42525	O42525	scylliorhinu	
228	3	10.7	28	13	Q90757	Q90757	gallus gall	

229	3	10.7	28	13	Q9DFT7	Q9dft7	gallus gall
230	3	10.7	28	15	Q73626	Q73626	human immun
231	3	10.7	28	15	O71995	O71995	human endog
232	3	10.7	28	15	Q70310	Q70310	human immun
233	3	10.7	28	16	Q8ENT7	Q8ent7	oceanobacil
234	3	10.7	28	16	Q8E014	Q8e014	streptococc
235	3	10.7	28	17	Q8ZYY3	Q8zyy3	pyrobaculum
236	3	10.7	29	2	Q93IG2	Q93ig2	thiobacillu
237	3	10.7	29	2	Q49148	Q49148	methylobact
238	3	10.7	29	2	Q9R526	Q9r526	vibrio chol
239	3	10.7	29	2	Q9R5G7	Q9r5g7	fusobacteri
240	3	10.7	29	2	Q9K340	Q9k340	vibrio chol
241	3	10.7	29	2	Q9ACD9	Q9acd9	vibrio salm
242	3	10.7	29	2	Q51692	Q51692	paracoccus
243	3	10.7	29	3	Q8TGQ5	Q8tgq5	saccharomyc
244	3	10.7	29	3	Q9HDQ3	Q9hdq3	candida rug
245	3	10.7	29	4	Q9Y3G1	Q9y3g1	homo sapien
246	3	10.7	29	4	Q9H2A1	Q9h2a1	homo sapien
247	3	10.7	29	4	Q9UEF0	Q9uef0	homo sapien
248	3	10.7	29	4	O95485	O95485	homo sapien
249	3	10.7	29	4	Q8TAI5	Q8tai5	homo sapien
250	3	10.7	29	5	Q967U3	Q967u3	schistocerc
251	3	10.7	29	5	Q24684	Q24684	dugesia tig
252	3	10.7	29	5	Q8T3E8	Q8t3e8	caenorhabdi
253	3	10.7	29	5	Q24688	Q24688	dugesia tig
254	3	10.7	29	5	Q95SE3	Q95se3	drosophila
255	3	10.7	29	5	Q967U4	Q967u4	schistocerc
256	3	10.7	29	5	Q24683	Q24683	dugesia tig
257	3	10.7	29	5	Q8T936	Q8t936	folsomia ca
258	3	10.7	29	5	Q24687	Q24687	dugesia tig
259	3	10.7	29	5	Q8ITD6	Q8itd6	schistosoma
260	3	10.7	29	6	Q9TRL6	Q9trl6	bos taurus
261	3	10.7	29	6	Q9TSY6	Q9tsy6	pan troglod
262	3	10.7	29	6	Q8SQD5	Q8sqd5	macaca mula
263	3	10.7	29	6	O62784	O62784	isoodon mac
264	3	10.7	29	7	Q8HWM0	Q8hwm0	homo sapien
265	3	10.7	29	8	Q9G651	Q9g651	otocryptis
266	3	10.7	29	9	Q9ZX23	Q9zx23	mycobacteri
267	3	10.7	29	10	P82193	P82193	spinacia ol
268	3	10.7	29	11	Q9QWM6	Q9qwm6	mus musculu
269	3	10.7	29	11	O88227	O88227	mus musculu
270	3	10.7	29	11	O88221	O88221	mus musculu
271	3	10.7	29	11	Q9Z2C0	Q9z2c0	mus musculu
272	3	10.7	29	11	Q91VE8	Q91ve8	mus musculu
273	3	10.7	29	11	Q8K362	Q8k362	mus musculu
274	3	10.7	29	11	Q64353	Q64353	mus musculu
275	3	10.7	29	11	O88225	O88225	mus musculu
276	3	10.7	29	11	O88214	O88214	mus musculu
277	3	10.7	29	11	Q9Z2C1	Q9z2c1	mus musculu
278	3	10.7	29	11	O88217	O88217	mus musculu
279	3	10.7	29	11	O70564	O70564	mus musculu
280	3	10.7	29	11	Q91UZ3	Q91uz3	mus musculu
281	3	10.7	29	11	O88218	O88218	mus musculu
282	3	10.7	29	11	Q9QWN1	Q9qwn1	mus musculu
283	3	10.7	29	11	O88223	O88223	mus musculu
284	3	10.7	29	11	Q99JY5	Q99jy5	mus musculu
285	3	10.7	29	11	O88220	O88220	mus musculu

286	3	10.7	29	11	O88215	O88215	mus musculu
287	3	10.7	29	11	Q8CGM8	Q8cgm8	mus musculu
288	3	10.7	29	12	Q86235	Q86235	human rotav
289	3	10.7	29	12	Q86232	Q86232	human rotav
290	3	10.7	29	12	Q86233	Q86233	human rotav
291	3	10.7	29	12	O56835	O56835	vibrio chol
292	3	10.7	29	12	Q86234	Q86234	human rotav
293	3	10.7	29	13	Q9PRF9	Q9prf9	brachydanio
294	3	10.7	29	13	Q91396	Q91396	gallus gall
295	3	10.7	29	13	O13043	O13043	scyliorhinu
296	3	10.7	29	13	Q90894	Q90894	gallus gall
297	3	10.7	29	13	Q8AX77	Q8ax77	oreochromis
298	3	10.7	29	13	Q8AX76	Q8ax76	oreochromis
299	3	10.7	29	15	P89816	P89816	human immun
300	3	10.7	29	15	Q69897	Q69897	human immun
301	3	10.7	29	15	Q9WG58	Q9wg58	chimpanzee
302	3	10.7	29	15	Q88078	Q88078	chimpanzee
303	3	10.7	29	15	P89821	P89821	human immun
304	3	10.7	29	16	Q9JZN6	Q9jzn6	neisseria m
305	3	10.7	29	16	Q99UH5	Q99uh5	staphylococ
306	3	10.7	29	16	Q8X3T7	Q8x3t7	escherichia
307	3	10.7	29	16	Q8X3T6	Q8x3t6	escherichia
308	3	10.7	29	16	Q8NWX8	Q8nwx8	staphylococ
309	3	10.7	29	16	O86497	O86497	streptomyce
310	3	10.7	29	16	Q8FZ68	Q8fz68	brucella su
311	3	10.7	30	2	Q9R887	Q9r887	chlamydia t
312	3	10.7	30	2	Q9R4N2	Q9r4n2	pseudomonas
313	3	10.7	30	2	Q9L8W9	Q9l8w9	streptomyce
314	3	10.7	30	2	Q9R4C2	Q9r4c2	wolinella s
315	3	10.7	30	2	Q9F7U1	Q9f7u1	helicobacte
316	3	10.7	30	2	Q9L8X1	Q9l8x1	streptomyce
317	3	10.7	30	2	Q9REI5	Q9rei5	acidiphiliu
318	3	10.7	30	2	Q8VUW9	Q8vuw9	staphylococ
319	3	10.7	30	2	Q52299	Q52299	pseudomonas
320	3	10.7	30	2	Q9ZG27	Q9zg27	chlamydia t
321	3	10.7	30	2	Q9R5Q3	Q9r5q3	leuconostoc
322	3	10.7	30	2	Q93GF6	Q93gf6	staphylococ
323	3	10.7	30	2	Q9R5K3	Q9r5k3	leptospira
324	3	10.7	30	2	Q9S014	Q9s014	borrelia bu
325	3	10.7	30	2	Q8KYT6	Q8kyt6	bacillus an
326	3	10.7	30	2	P83001	P83001	pseudomonas
327	3	10.7	30	2	Q8GJA5	Q8gja5	campylobact
328	3	10.7	30	3	Q9P817	Q9p817	candida alb
329	3	10.7	30	3	Q8TGM3	Q8tgm3	saccharomyc
330	3	10.7	30	3	Q8X1N5	Q8x1n5	hypocrea ni
331	3	10.7	30	3	Q8WZD3	Q8wzd3	trichoderma
332	3	10.7	30	3	Q8X1N4	Q8x1n4	hypocrea fl
333	3	10.7	30	3	Q02176	Q02176	geotrichum
334	3	10.7	30	4	P78460	P78460	homo sapien
335	3	10.7	30	4	Q9UMJ2	Q9umj2	homo sapien
336	3	10.7	30	4	Q8WUP3	Q8wup3	homo sapien
337	3	10.7	30	4	Q15980	Q15980	homo sapien
338	3	10.7	30	4	Q8IU66	Q8iu66	homo sapien
339	3	10.7	30	5	Q8SZJ6	Q8szj6	drosophila
340	3	10.7	30	5	Q967V3	Q967v3	lithobius f
341	3	10.7	30	5	Q25627	Q25627	onchocerca
342	3	10.7	30	5	Q967V0	Q967v0	lithobius f

343	3	10.7	30	5	Q967V1	Q967v1 lithobius f
344	3	10.7	30	6	Q8MJJ5	Q8mjj5 gorilla gor
345	3	10.7	30	7	Q9Y453	Q9y453 homo sapien
346	3	10.7	30	8	Q9MJF6	Q9mjf6 candida alb
347	3	10.7	30	8	Q8M0A1	Q8m0a1 bucorvus le
348	3	10.7	30	8	Q9T2T8	Q9t2t8 bos taurus
349	3	10.7	30	9	Q9T162	Q9t162 bacteriopha
350	3	10.7	30	10	Q42133	Q42133 arabidopsis
351	3	10.7	30	10	Q41490	Q41490 solanum tub
352	3	10.7	30	11	Q9QVC3	Q9qvc3 rattus sp.
353	3	10.7	30	11	Q9JHF4	Q9jhf4 rattus norv
354	3	10.7	30	11	O88549	O88549 mesocricetu
355	3	10.7	30	11	Q9WUS5	Q9wus5 mus musculu
356	3	10.7	30	11	Q99LC0	Q99lc0 mus musculu
357	3	10.7	30	11	Q9QV18	Q9qv18 rattus sp.
358	3	10.7	30	11	Q9WUS6	Q9wus6 mus musculu
359	3	10.7	30	11	Q9QV19	Q9qv19 rattus sp.
360	3	10.7	30	11	Q9WUS7	Q9wus7 mus musculu
361	3	10.7	30	12	Q02949	Q02949 beet wester
362	3	10.7	30	15	Q70350	Q70350 human immun
363	3	10.7	30	15	Q03514	Q03514 mouse intra
364	3	10.7	30	16	Q9X066	Q9x066 thermotoga
365	3	10.7	30	16	Q9KU55	Q9ku55 vibrio chol
366	3	10.7	30	16	Q9KQQ5	Q9kqq5 vibrio chol
367	3	10.7	30	16	Q9JWF4	Q9jwf4 neisseria m
368	3	10.7	30	16	Q97QV7	Q97qv7 streptococc
369	3	10.7	30	16	Q9K1W7	Q9k1w7 chlamydia p
370	3	10.7	30	16	Q8U566	Q8u566 agrobacteri
371	3	10.7	30	16	Q93RS7	Q93rs7 streptomyce
372	3	10.7	30	16	Q8G2I8	Q8g2i8 brucella su
373	3	10.7	30	16	Q8ECQ9	Q8ecq9 shewanella
374	3	10.7	30	16	Q8EAT6	Q8eat6 shewanella
375	3	10.7	30	16	Q8CTZ5	Q8ctz5 staphylococ
376	3	10.7	30	16	Q8CTE8	Q8cte8 staphylococ
377	3	10.7	30	16	Q8CT39	Q8ct39 staphylococ
378	3	10.7	30	16	Q8CKS9	Q8cks9 yersinia pe
379	3	10.7	30	17	Q8ZWV2	Q8zvw2 pyrobaculum
380	3	10.7	31	2	Q45547	Q45547 bacillus su
381	3	10.7	31	2	Q9L7N5	Q9l7n5 borrelia bi
382	3	10.7	31	2	Q9Z352	Q9z352 synechococc
383	3	10.7	31	2	Q52707	Q52707 rhodobacter
384	3	10.7	31	2	Q9JP49	Q9jp49 azospirillu
385	3	10.7	31	2	Q93GF7	Q93gf7 staphylococ
386	3	10.7	31	2	Q8KYP8	Q8kyp8 bacillus an
387	3	10.7	31	2	Q9L7N3	Q9l7n3 borrelia an
388	3	10.7	31	2	Q9RZY3	Q9rzy3 borrelia bu
389	3	10.7	31	2	Q9R4X1	Q9r4x1 treponema d
390	3	10.7	31	2	Q8RTS5	Q8rts5 uncultured
391	3	10.7	31	2	Q46662	Q46662 enterobacte
392	3	10.7	31	2	Q9L7N7	Q9l7n7 borrelia af
393	3	10.7	31	2	Q9R2G0	Q9r2g0 staphylococ
394	3	10.7	31	2	Q53411	Q53411 bacillus su
395	3	10.7	31	2	O52911	O52911 campylobact
396	3	10.7	31	3	Q8TGQ4	Q8tgq4 saccharomyc
397	3	10.7	31	3	Q9URA5	Q9ura5 candida alb
398	3	10.7	31	4	Q9UHE3	Q9uhe3 homo sapien
399	3	10.7	31	4	Q96FZ1	Q96fz1 homo sapien

400	3	10.7	31	4	Q9Y2A3	Q9y2a3 homo sapien
401	3	10.7	31	4	Q9UHM9	Q9uhm9 homo sapien
402	3	10.7	31	4	Q9UMS7	Q9ums7 homo sapien
403	3	10.7	31	4	Q9UD38	Q9ud38 homo sapien
404	3	10.7	31	5	Q8IQV3	Q8iqv3 drosophila
405	3	10.7	31	5	Q8IF28	Q8if28 trypanosoma
406	3	10.7	31	6	Q8MI94	Q8mi94 tupaia tana
407	3	10.7	31	6	Q8MIH5	Q8mih5 canis famil
408	3	10.7	31	6	Q8MIC3	Q8mic3 ochotona pr
409	3	10.7	31	6	Q8WP05	Q8wp05 ateles belz
410	3	10.7	31	6	Q8MIC9	Q8mic9 nycticebus
411	3	10.7	31	6	Q9GKL4	Q9gkl4 canis famil
412	3	10.7	31	6	Q8MIG4	Q8mig4 cynocephalu
413	3	10.7	31	6	Q9TSE4	Q9tse4 oryctolagus
414	3	10.7	31	8	Q9MS59	Q9ms59 euglena san
415	3	10.7	31	8	Q9MS62	Q9ms62 euglena myx
416	3	10.7	31	8	Q9MS74	Q9ms74 euglena ana
417	3	10.7	31	8	Q9MS68	Q9ms68 euglena des
418	3	10.7	31	8	Q9MS53	Q9ms53 euglena vir
419	3	10.7	31	8	Q9MS56	Q9ms56 euglena ste
420	3	10.7	31	8	Q9MS71	Q9ms71 lepocinclis
421	3	10.7	31	9	Q38402	Q38402 bacterioph
422	3	10.7	31	9	Q9B083	Q9b083 mycobacteri
423	3	10.7	31	10	Q9LEJ3	Q9lej3 glycine max
424	3	10.7	31	10	Q9AT70	Q9at70 coffea arab
425	3	10.7	31	10	Q8LKB4	Q8lkb4 musa acumin
426	3	10.7	31	10	Q9FUQ2	Q9fuq2 zea mays (s
427	3	10.7	31	11	Q8K1W2	Q8k1w2 cavia porce
428	3	10.7	31	11	Q99KK6	Q99kk6 mus musculu
429	3	10.7	31	11	O55182	O55182 rattus norv
430	3	10.7	31	11	Q9WUS8	Q9wus8 mus musculu
431	3	10.7	31	11	Q99PC8	Q99pc8 rattus norv
432	3	10.7	31	11	Q8K1P4	Q8k1p4 sciurus vul
433	3	10.7	31	12	Q919E5	Q919e5 human papil
434	3	10.7	31	12	Q919E4	Q919e4 human papil
435	3	10.7	31	12	Q919F7	Q919f7 human papil
436	3	10.7	31	12	Q919E6	Q919e6 human papil
437	3	10.7	31	12	Q919F3	Q919f3 human papil
438	3	10.7	31	12	Q919F8	Q919f8 human papil
439	3	10.7	31	12	Q919E1	Q919e1 human papil
440	3	10.7	31	12	Q919D9	Q919d9 human papil
441	3	10.7	31	12	Q919F6	Q919f6 human papil
442	3	10.7	31	12	Q919E3	Q919e3 human papil
443	3	10.7	31	12	Q919E8	Q919e8 human papil
444	3	10.7	31	12	Q919F0	Q919f0 human papil
445	3	10.7	31	12	Q919F4	Q919f4 human papil
446	3	10.7	31	12	Q69354	Q69354 herpes simp
447	3	10.7	31	12	Q919F2	Q919f2 human papil
448	3	10.7	31	12	Q919F1	Q919f1 human papil
449	3	10.7	31	12	Q919E2	Q919e2 human papil
450	3	10.7	31	12	Q919D8	Q919d8 human papil
451	3	10.7	31	12	Q919E9	Q919e9 human papil
452	3	10.7	31	12	Q919D7	Q919d7 human papil
453	3	10.7	31	12	Q919F5	Q919f5 human papil
454	3	10.7	31	12	Q919E0	Q919e0 human papil
455	3	10.7	31	12	Q919E7	Q919e7 human papil
456	3	10.7	31	13	Q9DFI9	Q9dfi9 monopterus

457	3	10.7	31	13	Q8JJ98	Q8jj98	melanoptila
458	3	10.7	31	13	Q8JJ93	Q8jj93	ramphocincl
459	3	10.7	31	13	Q8JJA3	Q8jja3	cinclocerth
460	3	10.7	31	13	Q91704	Q91704	xenopus lae
461	3	10.7	31	13	Q8JJA4	Q8jja4	cinclocerth
462	3	10.7	31	13	Q8JJ99	Q8jj99	margarops f
463	3	10.7	31	13	Q8JJA0	Q8jja0	margarops f
464	3	10.7	31	13	Q8JJ97	Q8jj97	melanotis c
465	3	10.7	31	13	Q8JJA1	Q8jja1	dumetella c
466	3	10.7	31	13	Q8JJ96	Q8jj96	mimus gilvu
467	3	10.7	31	15	Q87950	Q87950	chimpanzee
468	3	10.7	31	15	Q83937	Q83937	ovine lenti
469	3	10.7	31	16	O25108	O25108	helicobacte
470	3	10.7	31	16	Q9PAW4	Q9paw4	xylella fas
471	3	10.7	31	16	Q9PA95	Q9pa95	xylella fas
472	3	10.7	31	16	Q9KU30	Q9ku30	vibrio chol
473	3	10.7	31	16	Q9K7A8	Q9k7a8	bacillus ha
474	3	10.7	31	16	Q9K0T6	Q9k0t6	neisseria m
475	3	10.7	31	16	Q9JXQ7	Q9jxq7	neisseria m
476	3	10.7	31	16	Q97T66	Q97t66	streptococc
477	3	10.7	31	16	Q97SZ9	Q97sz9	streptococc
478	3	10.7	31	16	Q97QJ4	Q97qj4	streptococc
479	3	10.7	31	16	Q931I1	Q931i1	staphylococ
480	3	10.7	31	16	Q9K200	Q9k200	chlamydia p
481	3	10.7	31	16	Q8U567	Q8u567	agrobacteri
482	3	10.7	31	16	Q8VWC7	Q8vwc7	streptomyce
483	3	10.7	31	16	Q9ZK13	Q9zk13	helicobacte
484	3	10.7	31	16	Q8KF13	Q8kf13	chlorobium
485	3	10.7	31	16	Q8KEY3	Q8key3	chlorobium
486	3	10.7	31	16	Q8KCQ0	Q8kcq0	chlorobium
487	3	10.7	31	16	Q8KCG9	Q8kcg9	chlorobium
488	3	10.7	31	16	Q8KAG1	Q8kag1	chlorobium
489	3	10.7	31	16	Q8FYY1	Q8fyy1	brucella su
490	3	10.7	31	16	Q8EI77	Q8ei77	shewanella
491	3	10.7	31	16	Q8EHI1	Q8ehi1	shewanella
492	3	10.7	31	16	Q8EGZ1	Q8egz1	shewanella
493	3	10.7	31	16	Q8E9Y5	Q8e9y5	shewanella
494	3	10.7	31	16	Q8E2H9	Q8e2h9	streptococc
495	3	10.7	31	16	Q8DYE5	Q8dye5	streptococc
496	3	10.7	31	16	Q8CU39	Q8cu39	staphylococ
497	3	10.7	31	16	Q8CQQ0	Q8cq0	staphylococ
498	3	10.7	32	2	Q99224	Q99224	klebsiella
499	3	10.7	32	2	Q00491	Q00491	streptomyce
500	3	10.7	32	2	Q9KJE5	Q9kje5	thauera aro
501	3	10.7	32	2	Q8VU88	Q8vu88	lactobacill
502	3	10.7	32	2	Q9Z639	Q9z639	streptococc
503	3	10.7	32	2	Q9Z638	Q9z638	streptococc
504	3	10.7	32	2	Q8VN21	Q8vn21	kluuyvera ci
505	3	10.7	32	2	Q9R5X1	Q9r5x1	bordetella
506	3	10.7	32	2	Q49137	Q49137	methylobact
507	3	10.7	32	2	Q9APT5	Q9apt5	pseudomonas
508	3	10.7	32	2	Q8VNT6	Q8vnt6	enterobacte
509	3	10.7	32	2	Q47227	Q47227	escherichia
510	3	10.7	32	2	Q51855	Q51855	pasteurella
511	3	10.7	32	3	Q9URU5	Q9uru5	schizosacch
512	3	10.7	32	3	Q8TGR9	Q8tgr9	saccharomyc
513	3	10.7	32	4	Q96RK7	Q96rk7	homo sapien

514	3	10.7	32	4	Q9BY35	Q9by35 homo sapien
515	3	10.7	32	4	Q9UEB0	Q9ueb0 homo sapien
516	3	10.7	32	4	Q8TB02	Q8tb02 homo sapien
517	3	10.7	32	4	Q9HAX8	Q9hax8 homo sapien
518	3	10.7	32	4	Q8TBQ3	Q8tbq3 homo sapien
519	3	10.7	32	4	Q96D66	Q96d66 homo sapien
520	3	10.7	32	4	Q8NG01	Q8ng01 homo sapien
521	3	10.7	32	4	Q9UNE9	Q9une9 homo sapien
522	3	10.7	32	5	Q9GPD9	Q9gpd9 drosophila
523	3	10.7	32	5	Q9GTB1	Q9gtb1 eimeria ten
524	3	10.7	32	5	Q26651	Q26651 strongyloce
525	3	10.7	32	5	Q26828	Q26828 trypanosoma
526	3	10.7	32	5	Q8T382	Q8t382 leishmania
527	3	10.7	32	5	O96634	O96634 trypanosoma
528	3	10.7	32	5	Q9GNH0	Q9gnh0 drosophila
529	3	10.7	32	5	Q9GT99	Q9gt99 babesia bov
530	3	10.7	32	5	Q9GTC0	Q9gtc0 neospora ca
531	3	10.7	32	6	Q9TSE6	Q9tse6 oryctolagus
532	3	10.7	32	6	O62854	O62854 oryctolagus
533	3	10.7	32	6	Q9MYR8	Q9myr8 oryctolagus
534	3	10.7	32	6	Q9TSE5	Q9tse5 oryctolagus
535	3	10.7	32	6	O77647	O77647 macropus eu
536	3	10.7	32	7	Q95HL3	Q95hl3 homo sapien
537	3	10.7	32	7	Q8SNB9	Q8snb9 homo sapien
538	3	10.7	32	7	Q31597	Q31597 xenopus lae
539	3	10.7	32	7	Q9BCT8	Q9bct8 homo sapien
540	3	10.7	32	7	Q8MHQ2	Q8mhq2 homo sapien
541	3	10.7	32	7	Q9BCU0	Q9bcu0 homo sapien
542	3	10.7	32	8	Q94VL5	Q94vl5 salmo trutt
543	3	10.7	32	8	Q94NY1	Q94ny1 salmo salar
544	3	10.7	32	8	Q36463	Q36463 onychomys l
545	3	10.7	32	8	Q9T2Q1	Q9t2q1 pinus sylve
546	3	10.7	32	8	Q951P3	Q951p3 salmo salar
547	3	10.7	32	9	Q9MBU5	Q9mbu5 chlamydia p
548	3	10.7	32	9	Q9MBU9	Q9mbu9 vibrio phag
549	3	10.7	32	10	Q9S8X7	Q9s8x7 daucus caro
550	3	10.7	32	10	Q9FUQ1	Q9fuq1 zea mays (s
551	3	10.7	32	10	Q9FUQ4	Q9fuq4 zea mays (s
552	3	10.7	32	10	Q9FE80	Q9fe80 zea diplope
553	3	10.7	32	10	Q9FUP8	Q9fup8 zea luxuria
554	3	10.7	32	11	Q9R0E3	Q9r0e3 mus musculu
555	3	10.7	32	11	Q9QVG6	Q9qvg6 rattus sp.
556	3	10.7	32	11	P97642	P97642 rattus norv
557	3	10.7	32	11	Q61695	Q61695 mus musculu
558	3	10.7	32	11	Q9QWN2	Q9qwn2 mus musculu
559	3	10.7	32	11	P97649	P97649 rattus norv
560	3	10.7	32	11	Q8C2N8	Q8c2n8 mus musculu
561	3	10.7	32	11	Q8BS12	Q8bs12 mus musculu
562	3	10.7	32	12	Q66855	Q66855 foot-and-mo
563	3	10.7	32	13	Q8QG73	Q8qg73 oncorhynch
564	3	10.7	32	13	Q8QG72	Q8qg72 salmo salar
565	3	10.7	32	13	Q8QG71	Q8qg71 oncorhynch
566	3	10.7	32	13	Q9PS21	Q9ps21 carassius a
567	3	10.7	32	13	Q8UUN6	Q8uun6 xenopus lae
568	3	10.7	32	13	Q8QG84	Q8qg84 oncorhynch
569	3	10.7	32	13	Q8QG83	Q8qg83 oncorhynch
570	3	10.7	32	13	Q8QG82	Q8qg82 oncorhynch

571	3	10.7	32	13	Q8QG70	Q8qg70	salvelinus
572	3	10.7	32	13	P82780	P82780	rana catesb
573	3	10.7	32	13	Q9W7P3	Q9w7p3	morone saxa
574	3	10.7	32	13	Q9W7P2	Q9w7p2	morone saxa
575	3	10.7	32	16	O50851	O50851	borrelia bu
576	3	10.7	32	16	Q9PCD4	Q9pcd4	xylella fas
577	3	10.7	32	16	Q9KVF7	Q9kvf7	vibrio chol
578	3	10.7	32	16	Q9KTM5	Q9ktm5	vibrio chol
579	3	10.7	32	16	Q9KKU3	Q9kku3	vibrio chol
580	3	10.7	32	16	Q9K6N3	Q9k6n3	bacillus ha
581	3	10.7	32	16	Q9K175	Q9k175	neisseria m
582	3	10.7	32	16	Q97SW9	Q97sw9	streptococc
583	3	10.7	32	16	Q97RT9	Q97rt9	streptococc
584	3	10.7	32	16	Q97NT4	Q97nt4	streptococc
585	3	10.7	32	16	Q8VKF9	Q8vkf9	mycobacteri
586	3	10.7	32	16	Q9CDK7	Q9cdk7	lactococcus
587	3	10.7	32	16	Q8KCV0	Q8kcv0	chlorobium
588	3	10.7	32	16	Q8KCP1	Q8kcp1	chlorobium
589	3	10.7	32	16	Q8EFA5	Q8efa5	shewanella
590	3	10.7	32	16	Q8ECK5	Q8eck5	shewanella
591	3	10.7	32	16	Q8E9X5	Q8e9x5	shewanella
592	3	10.7	32	16	Q8E9D2	Q8e9d2	shewanella
593	3	10.7	32	16	Q8CTI0	Q8cti0	staphylococ
594	3	10.7	32	16	Q8CTH2	Q8cth2	staphylococ
595	3	10.7	32	17	Q8ZZF7	Q8zzf7	pyrobaculum
596	3	10.7	33	1	Q9UWL4	Q9uwl4	methanopyru
597	3	10.7	33	2	Q9S3I9	Q9s3i9	haemophilus
598	3	10.7	33	2	Q9R5N9	Q9r5n9	clostridium
599	3	10.7	33	2	Q9K370	Q9k370	rhizobium l
600	3	10.7	33	2	Q9R2F6	Q9r2f6	klebsiella
601	3	10.7	33	2	Q9S3N5	Q9s3n5	bacillus ce
602	3	10.7	33	2	Q9ZG76	Q9zg76	chlamydia t
603	3	10.7	33	2	Q9KI23	Q9ki23	helicobacte
604	3	10.7	33	2	Q56122	Q56122	salmonella
605	3	10.7	33	2	Q09122	Q09122	fusobacteri
606	3	10.7	33	2	P82583	P82583	streptococc
607	3	10.7	33	2	Q8GQU2	Q8gqu2	leptospira
608	3	10.7	33	2	Q8GG98	Q8gg98	neisseria p
609	3	10.7	33	3	Q8TGR1	Q8tgr1	saccharomyc
610	3	10.7	33	3	Q10986	Q10986	absidia. ba
611	3	10.7	33	4	Q9NPZ1	Q9npz1	homo sapien
612	3	10.7	33	4	Q9BUZ1	Q9buz1	homo sapien
613	3	10.7	33	4	Q15285	Q15285	homo sapien
614	3	10.7	33	4	Q9UMG4	Q9umg4	homo sapien
615	3	10.7	33	4	Q9BST3	Q9bst3	homo sapien
616	3	10.7	33	4	Q9BV16	Q9bv16	homo sapien
617	3	10.7	33	4	Q8WWE0	Q8wwe0	homo sapien
618	3	10.7	33	4	Q9BYF4	Q9byf4	homo sapien
619	3	10.7	33	4	Q92668	Q92668	homo sapien
620	3	10.7	33	5	Q25433	Q25433	molgula cit
621	3	10.7	33	5	Q9GTB6	Q9gtb6	eimeria ten
622	3	10.7	33	5	Q9GT96	Q9gt96	cryptospori
623	3	10.7	33	5	Q9GTA3	Q9gta3	babesia bov
624	3	10.7	33	5	Q9GTB0	Q9gtb0	sarcocystis
625	3	10.7	33	5	Q27637	Q27637	drosophila
626	3	10.7	33	5	Q8WTH4	Q8wth4	heteroptery
627	3	10.7	33	5	Q9NGN0	Q9ngn0	strongyloce

628	3	10.7	33	5	Q9GTA7	Q9gta7 sarcocystis
629	3	10.7	33	5	Q9GTB8	Q9gtb8 neospora ca
630	3	10.7	33	5	Q9GTA5	Q9gta5 babesia bov
631	3	10.7	33	5	Q95S45	Q95s45 drosophila
632	3	10.7	33	5	Q9GT98	Q9gt98 cryptospori
633	3	10.7	33	5	O17147	O17147 echinococcu
634	3	10.7	33	5	Q9VHD7	Q9vhd7 drosophila
635	3	10.7	33	6	Q28788	Q28788 papio hamad
636	3	10.7	33	6	O77664	O77664 sus scrofa
637	3	10.7	33	6	Q9TSX7	Q9tsx7 sus scrofa
638	3	10.7	33	6	Q29066	Q29066 sus scrofa
639	3	10.7	33	6	Q9TRD6	Q9trd6 oryctolagus
640	3	10.7	33	6	Q8MIL2	Q8mil2 bos taurus
641	3	10.7	33	8	Q9BAC6	Q9bac6 euglena gra
642	3	10.7	33	8	Q9BAC1	Q9bac1 euglena ste
643	3	10.7	33	8	Q8WI31	Q8wi31 psilotum nu
644	3	10.7	33	8	Q9BAC4	Q9bac4 euglena mut
645	3	10.7	33	8	Q9MS75	Q9ms75 euglena ana
646	3	10.7	33	8	O47024	O47024 barbeya ole
647	3	10.7	33	9	Q8SCC2	Q8scc2 vibrio harv
648	3	10.7	33	9	Q38588	Q38588 bacterioph
649	3	10.7	33	9	Q38551	Q38551 bacterioph
650	3	10.7	33	10	Q02904	Q02904 arabidopsis
651	3	10.7	33	10	Q94IJ2	Q94ij2 zea mays (m
652	3	10.7	33	10	Q9XJ70	Q9xj70 cucumis sat
653	3	10.7	33	10	Q9AYQ5	Q9ayq5 cucumis sat
654	3	10.7	33	10	Q9XJ69	Q9xj69 cucumis sat
655	3	10.7	33	10	Q8H7H6	Q8h7h6 arabidopsis
656	3	10.7	33	11	O88226	O88226 mus musculu
657	3	10.7	33	11	Q9JLA8	Q9jla8 mus musculu
658	3	10.7	33	11	Q9Z298	Q9z298 rattus norv
659	3	10.7	33	11	Q9QVM2	Q9qvm2 mus sp. glu
660	3	10.7	33	11	P97670	P97670 rattus norv
661	3	10.7	33	11	Q62539	Q62539 mus spretus
662	3	10.7	33	12	O72982	O72982 hepatitis c
663	3	10.7	33	12	O73068	O73068 hepatitis c
664	3	10.7	33	12	O72979	O72979 hepatitis c
665	3	10.7	33	12	O72988	O72988 hepatitis c
666	3	10.7	33	12	O72992	O72992 hepatitis c
667	3	10.7	33	12	O72990	O72990 hepatitis c
668	3	10.7	33	12	O73010	O73010 hepatitis c
669	3	10.7	33	12	O72981	O72981 hepatitis c
670	3	10.7	33	12	O09759	O09759 lettuce mos
671	3	10.7	33	12	Q65687	Q65687 bovine papi
672	3	10.7	33	12	O73008	O73008 hepatitis c
673	3	10.7	33	12	O72986	O72986 hepatitis c
674	3	10.7	33	12	O72993	O72993 hepatitis c
675	3	10.7	33	12	O72984	O72984 hepatitis c
676	3	10.7	33	12	O73005	O73005 hepatitis c
677	3	10.7	33	12	O73067	O73067 hepatitis c
678	3	10.7	33	12	O72985	O72985 hepatitis c
679	3	10.7	33	12	Q9PXQ9	Q9pxq9 tobacco mos
680	3	10.7	33	12	O72983	O72983 hepatitis c
681	3	10.7	33	12	O72987	O72987 hepatitis c
682	3	10.7	33	12	Q69461	Q69461 human herpe
683	3	10.7	33	12	O72978	O72978 hepatitis c
684	3	10.7	33	12	O73009	O73009 hepatitis c

685	3	10.7	33	13	Q9DD87	Q9dd87	brachyramph
686	3	10.7	33	13	Q9PT34	Q9pt34	oncorhynch
687	3	10.7	33	13	Q8UUR8	Q8uur8	brachydanio
688	3	10.7	33	13	Q9DD86	Q9dd86	brachyramph
689	3	10.7	33	13	Q9W7N9	Q9w7n9	morone saxa
690	3	10.7	33	15	Q9DZ98	Q9dz98	human immun
691	3	10.7	33	15	Q9QKI9	Q9qki9	human immun
692	3	10.7	33	15	Q8QDU0	Q8qdu0	human immun
693	3	10.7	33	15	Q70443	Q70443	human immun
694	3	10.7	33	15	Q8QDT9	Q8qdt9	human immun
695	3	10.7	33	15	Q9PXE1	Q9pxe1	human immun
696	3	10.7	33	16	O25518	O25518	helicobacte
697	3	10.7	33	16	O50777	O50777	borrelia bu
698	3	10.7	33	16	Q9KSG4	Q9ksg4	vibrio chol
699	3	10.7	33	16	Q9KRR7	Q9krr7	vibrio chol
700	3	10.7	33	16	Q9KQP4	Q9kqp4	vibrio chol
701	3	10.7	33	16	Q9JY44	Q9jy44	neisseria m
702	3	10.7	33	16	Q9JUM4	Q9jum4	neisseria m
703	3	10.7	33	16	Q9A388	Q9a388	caulobacter
704	3	10.7	33	16	Q8VK01	Q8vk01	mycobacteri
705	3	10.7	33	16	Q8VJK1	Q8vjk1	mycobacteri
706	3	10.7	33	16	Q8NT95	Q8nt95	corynebacte
707	3	10.7	33	16	Q8NLP2	Q8nlp2	corynebacte
708	3	10.7	33	16	Q8KG99	Q8kg99	chlorobium
709	3	10.7	33	16	Q8KE00	Q8ke00	chlorobium
710	3	10.7	33	16	Q8KBZ0	Q8kbz0	chlorobium
711	3	10.7	33	16	Q8G1K3	Q8g1k3	brucella su
712	3	10.7	33	16	Q8G173	Q8g173	brucella su
713	3	10.7	33	16	Q8G0U8	Q8g0u8	brucella su
714	3	10.7	33	16	Q8FYD4	Q8fyd4	brucella su
715	3	10.7	33	16	Q8FSG0	Q8fsg0	corynebacte
716	3	10.7	33	16	Q8EHN3	Q8ehn3	shewanella
717	3	10.7	33	16	Q8EFM7	Q8efm7	shewanella
718	3	10.7	33	16	Q8EEJ9	Q8eej9	shewanella
719	3	10.7	33	16	Q8ECS9	Q8ecs9	shewanella
720	3	10.7	33	16	Q8E877	Q8e877	shewanella
721	3	10.7	33	16	Q8DWK4	Q8dwk4	streptococc
722	3	10.7	33	16	Q8CTR8	Q8ctr8	staphylococ
723	3	10.7	33	17	Q9HSX6	Q9hsx6	halobacteri
724	3	10.7	34	1	Q9P9L8	Q9p9l8	methanosarc
725	3	10.7	34	2	Q8KYQ3	Q8kyq3	bacillus an
726	3	10.7	34	2	Q02571	Q02571	klebsiella
727	3	10.7	34	2	Q8KJV6	Q8kjb6	proteus vul
728	3	10.7	34	2	Q50998	Q50998	neisseria g
729	3	10.7	34	2	Q43910	Q43910	azospirillu
730	3	10.7	34	2	Q51131	Q51131	neisseria m
731	3	10.7	34	2	Q8KYH2	Q8kyh2	bacillus an
732	3	10.7	34	2	Q9KWG7	Q9kwg7	citrobacter
733	3	10.7	34	2	Q53594	Q53594	streptomyce
734	3	10.7	34	2	Q9RZW6	Q9rzw6	borrelia bu
735	3	10.7	34	2	Q9R885	Q9r885	chlamydia t
736	3	10.7	34	2	Q9L3B8	Q9l3b8	mycobacteri
737	3	10.7	34	2	Q8GGA4	Q8gga4	neisseria l
738	3	10.7	34	4	Q8WY57	Q8wy57	homo sapien
739	3	10.7	34	4	Q8WW51	Q8ww51	homo sapien
740	3	10.7	34	4	Q9BXC5	Q9bxc5	homo sapien
741	3	10.7	34	4	Q9H530	Q9h530	homo sapien

742	3	10.7	34	4	Q9UCI7	Q9uci7 homo sapien
743	3	10.7	34	4	Q8WYN8	Q8wyn8 homo sapien
744	3	10.7	34	4	Q96Q75	Q96q75 homo sapien
745	3	10.7	34	4	Q96C21	Q96c21 homo sapien
746	3	10.7	34	4	Q9UCJ5	Q9ucj5 homo sapien
747	3	10.7	34	4	Q9BU51	Q9bu51 homo sapien
748	3	10.7	34	4	Q96C89	Q96c89 homo sapien
749	3	10.7	34	5	Q8T3M2	Q8t3m2 drosophila
750	3	10.7	34	5	Q9BIQ3	Q9biq3 cooperia pu
751	3	10.7	34	5	Q9BIQ1	Q9biq1 cooperia pu
752	3	10.7	34	5	Q27821	Q27821 trichomonas
753	3	10.7	34	5	Q8WTH8	Q8wth8 ctenomorpho
754	3	10.7	34	5	Q9GN73	Q9gn73 drosophila
755	3	10.7	34	5	Q9BIQ2	Q9biq2 cooperia pu
756	3	10.7	34	5	Q9GQE5	Q9gqe5 branchiosto
757	3	10.7	34	5	Q9BIQ0	Q9biq0 cooperia pu
758	3	10.7	34	5	Q9GN69	Q9gn69 drosophila
759	3	10.7	34	5	Q8WTF8	Q8wtf8 sialis hama
760	3	10.7	34	5	Q9TWU9	Q9twu9 schistocerc
761	3	10.7	34	5	Q8INS3	Q8ins3 drosophila
762	3	10.7	34	6	Q29225	Q29225 sus scrofa
763	3	10.7	34	6	Q9TS91	Q9ts91 oryctolagus
764	3	10.7	34	6	Q8SPN7	Q8spn7 macaca mula
765	3	10.7	34	6	Q9TRI2	Q9tri2 sus scrofa
766	3	10.7	34	6	Q29351	Q29351 sus scrofa
767	3	10.7	34	6	Q29299	Q29299 sus scrofa
768	3	10.7	34	7	Q29863	Q29863 homo sapien
769	3	10.7	34	8	Q9T2T7	Q9t2t7 bos taurus
770	3	10.7	34	8	Q95A06	Q95a06 ophisurus m
771	3	10.7	34	8	Q8MCA2	Q8mca2 phaseolus a
772	3	10.7	34	8	Q9XNP0	Q9xnp0 boophilus m
773	3	10.7	34	9	Q8SCC1	Q8scc1 vibrio harv
774	3	10.7	34	10	Q41589	Q41589 triticum ae
775	3	10.7	34	10	Q43108	Q43108 pteris vitt
776	3	10.7	34	11	O35471	O35471 mus musculu
777	3	10.7	34	11	Q91Y56	Q91y56 mus musculu
778	3	10.7	34	11	Q9ET72	Q9et72 mus musculu
779	3	10.7	34	11	Q64344	Q64344 rattus norv
780	3	10.7	34	11	Q64115	Q64115 rattus sp.
781	3	10.7	34	11	Q9CV73	Q9cv73 mus musculu
782	3	10.7	34	11	P97647	P97647 rattus norv
783	3	10.7	34	11	Q62534	Q62534 mus spretus
784	3	10.7	34	11	Q62535	Q62535 mus spretus
785	3	10.7	34	11	Q9WUU0	Q9wuu0 mus musculu
786	3	10.7	34	11	Q8C4P4	Q8c4p4 mus musculu
787	3	10.7	34	12	Q9E8K5	Q9e8k5 hepatitis b
788	3	10.7	34	12	Q69212	Q69212 human cytom
789	3	10.7	34	13	Q8QGF9	Q8qgf9 oncorhynchu
790	3	10.7	34	13	Q8QGG2	Q8qgg2 oncorhynchu
791	3	10.7	34	13	Q9DDE8	Q9dde8 clarias gar
792	3	10.7	34	13	Q8QFM9	Q8qfm9 oncorhynchu
793	3	10.7	34	13	Q8QGG1	Q8qgg1 oncorhynchu
794	3	10.7	34	13	Q8QGF7	Q8qgf7 oncorhynchu
795	3	10.7	34	13	Q98TM8	Q98tm8 platichthys
796	3	10.7	34	13	Q8QGG0	Q8qgg0 oncorhynchu
797	3	10.7	34	15	Q79493	Q79493 human immun
798	3	10.7	34	15	Q72952	Q72952 human immun

799	3	10.7	34	15	091361	091361	human	immun
800	3	10.7	34	15	071801	071801	human	immun
801	3	10.7	34	15	071805	071805	human	immun
802	3	10.7	34	15	091357	091357	human	immun
803	3	10.7	34	15	Q9QQZ2	Q9qqz2	human	immun
804	3	10.7	34	15	P90368	P90368	human	immun
805	3	10.7	34	15	Q72953	Q72953	human	immun
806	3	10.7	34	15	071743	071743	human	immun
807	3	10.7	34	15	Q9QR24	Q9qr24	human	immun
808	3	10.7	34	15	091368	091368	human	immun
809	3	10.7	34	15	071728	071728	human	immun
810	3	10.7	34	15	071730	071730	human	immun
811	3	10.7	34	15	Q80484	Q80484	human	immun
812	3	10.7	34	15	Q80604	Q80604	human	immun
813	3	10.7	34	15	Q79463	Q79463	human	immun
814	3	10.7	34	15	Q97619	Q97619	human	immun
815	3	10.7	34	15	071817	071817	human	immun
816	3	10.7	34	15	071802	071802	human	immun
817	3	10.7	34	15	091360	091360	human	immun
818	3	10.7	34	15	071804	071804	human	immun
819	3	10.7	34	15	071813	071813	human	immun
820	3	10.7	34	15	071724	071724	human	immun
821	3	10.7	34	15	091355	091355	human	immun
822	3	10.7	34	15	071744	071744	human	immun
823	3	10.7	34	15	091356	091356	human	immun
824	3	10.7	34	15	Q97637	Q97637	human	immun
825	3	10.7	34	15	Q8J3W7	Q8j3w7	human	immun
826	3	10.7	34	15	Q76341	Q76341	human	immun
827	3	10.7	34	15	071816	071816	human	immun
828	3	10.7	34	15	Q97651	Q97651	human	immun
829	3	10.7	34	15	071745	071745	human	immun
830	3	10.7	34	15	091364	091364	human	immun
831	3	10.7	34	15	091369	091369	human	immun
832	3	10.7	34	15	Q9W8Y1	Q9w8y1	chimpanzee	
833	3	10.7	34	15	Q97649	Q97649	human	immun
834	3	10.7	34	15	Q8J3X2	Q8j3x2	human	immun
835	3	10.7	34	15	071734	071734	human	immun
836	3	10.7	34	15	071746	071746	human	immun
837	3	10.7	34	15	091365	091365	human	immun
838	3	10.7	34	15	091367	091367	human	immun
839	3	10.7	34	15	Q97616	Q97616	human	immun
840	3	10.7	34	15	071821	071821	human	immun
841	3	10.7	34	15	Q8QDV6	Q8qdv6	human	immun
842	3	10.7	34	15	091358	091358	human	immun
843	3	10.7	34	15	091363	091363	human	immun
844	3	10.7	34	15	091359	091359	human	immun
845	3	10.7	34	15	071829	071829	human	immun
846	3	10.7	34	15	Q76345	Q76345	human	immun
847	3	10.7	34	15	071742	071742	human	immun
848	3	10.7	34	15	071831	071831	human	immun
849	3	10.7	34	15	091354	091354	human	immun
850	3	10.7	34	15	Q8QDU9	Q8qdu9	human	immun
851	3	10.7	34	15	071811	071811	human	immun
852	3	10.7	34	15	071809	071809	human	immun
853	3	10.7	34	15	Q9WR33	Q9wr33	human	immun
854	3	10.7	34	15	071757	071757	human	immun
855	3	10.7	34	15	091362	091362	human	immun

856	3	10.7	34	15	O71814	O71814 human immun
857	3	10.7	34	15	Q97618	Q97618 human immun
858	3	10.7	34	15	O71731	O71731 human immun
859	3	10.7	34	15	Q97617	Q97617 human immun
860	3	10.7	34	15	Q78211	Q78211 human immun
861	3	10.7	34	15	O71796	O71796 human immun
862	3	10.7	34	16	O25955	O25955 helicobacte
863	3	10.7	34	16	O50720	O50720 borrelia bu
864	3	10.7	34	16	O50785	O50785 borrelia bu
865	3	10.7	34	16	O50799	O50799 borrelia bu
866	3	10.7	34	16	O50839	O50839 borrelia bu
867	3	10.7	34	16	O51026	O51026 borrelia bu
868	3	10.7	34	16	Q9PGF8	Q9pgf8 xylella fas
869	3	10.7	34	16	Q9PFA5	Q9pfa5 xylella fas
870	3	10.7	34	16	Q9KQ46	Q9kq46 vibrio chol
871	3	10.7	34	16	Q9KM63	Q9km63 vibrio chol
872	3	10.7	34	16	Q9K0X6	Q9k0x6 neisseria m
873	3	10.7	34	16	Q9JY24	Q9jy24 neisseria m
874	3	10.7	34	16	Q9JUR9	Q9jur9 neisseria m
875	3	10.7	34	16	Q97P56	Q97p56 streptococc
876	3	10.7	34	16	Q97K50	Q97k50 clostridium
877	3	10.7	34	16	Q9K2B9	Q9k2b9 chlamydia p
878	3	10.7	34	16	Q8XVG6	Q8xvg6 ralstonia s
879	3	10.7	34	16	Q8X457	Q8x457 escherichia
880	3	10.7	34	16	Q8KFH3	Q8kfh3 chlorobium
881	3	10.7	34	16	Q8KE71	Q8ke71 chlorobium
882	3	10.7	34	16	Q8KBR4	Q8kbr4 chlorobium
883	3	10.7	34	16	Q9S2B7	Q9s2b7 streptomyce
884	3	10.7	34	16	Q8G2Q2	Q8g2q2 brucella su
885	3	10.7	34	16	Q8F9A8	Q8f9a8 leptospira
886	3	10.7	34	16	Q8F6G1	Q8f6g1 leptospira
887	3	10.7	34	16	Q8F507	Q8f507 leptospira
888	3	10.7	34	16	Q8F423	Q8f423 leptospira
889	3	10.7	34	16	Q8F2W2	Q8f2w2 leptospira
890	3	10.7	34	16	Q8F2G7	Q8f2g7 leptospira
891	3	10.7	34	16	Q8F1Y9	Q8f1y9 leptospira
892	3	10.7	34	16	Q8F0V9	Q8f0v9 leptospira
893	3	10.7	34	16	Q8F0G8	Q8f0g8 leptospira
894	3	10.7	34	16	Q8EZ37	Q8ez37 leptospira
895	3	10.7	34	16	Q8EYP4	Q8eyp4 leptospira
896	3	10.7	34	16	Q8EXY2	Q8exy2 leptospira
897	3	10.7	34	16	Q8EXH8	Q8exh8 leptospira
898	3	10.7	34	16	Q8EXH6	Q8exh6 leptospira
899	3	10.7	34	16	Q8EHS0	Q8ehs0 shewanella
900	3	10.7	34	16	Q8EHK1	Q8ehk1 shewanella
901	3	10.7	34	16	Q8EBU4	Q8ebu4 shewanella
902	3	10.7	34	16	Q8E8Y3	Q8e8y3 shewanella
903	3	10.7	34	16	Q8DZH8	Q8dzh8 streptococc
904	3	10.7	34	16	Q8CTV6	Q8ctv6 staphylococ
905	3	10.7	34	16	Q8CTU8	Q8ctu8 staphylococ
906	3	10.7	34	16	Q8CLE7	Q8cle7 yersinia pe
907	3	10.7	35	2	Q9ZGU9	Q9zgu9 escherichia
908	3	10.7	35	2	O33758	O33758 streptococc
909	3	10.7	35	2	O87904	O87904 coxiella bu
910	3	10.7	35	2	Q9R4Z3	Q9r4z3 lactobacill
911	3	10.7	35	2	Q9RPW0	Q9rpw0 bacillus me
912	3	10.7	35	2	O30661	O30661 vibrio chol

913	3	10.7	35	2	Q48442	Q48442 klebsiella
914	3	10.7	35	2	Q9ZG68	Q9zg68 chlamydia t
915	3	10.7	35	2	Q8RTK5	Q8rtk5 leuconostoc
916	3	10.7	35	3	Q9URA2	Q9ura2 trametes ve
917	3	10.7	35	3	Q9UR84	Q9ur84 penicillium
918	3	10.7	35	3	Q9URA3	Q9ura3 trametes ve
919	3	10.7	35	3	Q8TGS4	Q8tgs4 saccharomyc
920	3	10.7	35	4	Q9BS62	Q9bs62 homo sapien
921	3	10.7	35	4	Q16157	Q16157 homo sapien
922	3	10.7	35	4	Q14530	Q14530 homo sapien
923	3	10.7	35	4	Q14844	Q14844 homo sapien
924	3	10.7	35	5	Q17349	Q17349 caenorhabdi
925	3	10.7	35	5	Q27754	Q27754 pisaster oc
926	3	10.7	35	5	Q8WTG4	Q8wtg4 oreophoetes
927	3	10.7	35	5	Q26372	Q26372 tribolium c
928	3	10.7	35	5	Q9BHK9	Q9bhk9 caenorhabdi
929	3	10.7	35	5	Q8IF25	Q8if25 trypanosoma
930	3	10.7	35	6	Q18877	Q18877 canis famil
931	3	10.7	35	6	Q95N74	Q95n74 equus cabal
932	3	10.7	35	8	Q8M1P5	Q8mlp5 nirridessus
933	3	10.7	35	8	Q95766	Q95766 cerataphis
934	3	10.7	35	8	Q04330	Q04330 candida par
935	3	10.7	35	8	Q8WEJ7	Q8wej7 cycas circi
936	3	10.7	35	8	Q62956	Q62956 picea abies
937	3	10.7	35	8	Q95A00	Q95a00 nemichthys
938	3	10.7	35	9	Q38294	Q38294 lactococcus
939	3	10.7	35	9	Q38508	Q38508 bacterioph
940	3	10.7	35	10	P92971	P92971 arabidopsis
941	3	10.7	35	10	Q8L986	Q8l986 arabidopsis
942	3	10.7	35	10	Q94IS4	Q94is4 pinus radia
943	3	10.7	35	10	Q9S9I1	Q9s9i1 daucus caro
944	3	10.7	35	10	Q9SF57	Q9sf57 arabidopsis
945	3	10.7	35	10	Q8GUX3	Q8gux3 picea maria
946	3	10.7	35	10	Q8GUX2	Q8gux2 picea maria
947	3	10.7	35	10	Q8GUX0	Q8gux0 picea maria
948	3	10.7	35	10	Q8GUW8	Q8guw8 picea maria
949	3	10.7	35	10	Q8GS04	Q8gs04 arabidopsis
950	3	10.7	35	11	Q63896	Q63896 mus sp. nk-
951	3	10.7	35	11	Q63397	Q63397 rattus norv
952	3	10.7	35	11	Q55083	Q55083 mus musculu
953	3	10.7	35	11	Q8K1C8	Q8k1c8 mus musculu
954	3	10.7	35	11	Q60608	Q60608 mus musculu
955	3	10.7	35	11	Q9QV50	Q9qv50 rattus sp.
956	3	10.7	35	11	P97643	P97643 rattus norv
957	3	10.7	35	11	Q9Z2G3	Q9z2g3 rattus norv
958	3	10.7	35	11	Q9R086	Q9r086 mus musculu
959	3	10.7	35	11	Q9QVT2	Q9qvt2 mus sp. ret
960	3	10.7	35	11	Q8CC11	Q8cc11 mus musculu
961	3	10.7	35	12	Q9YR05	Q9yr05 porcine cir
962	3	10.7	35	12	Q9YQW9	Q9yqw9 porcine cir
963	3	10.7	35	12	Q91864	Q91864 porcine cir
964	3	10.7	35	12	Q91HA8	Q91ha8 porcine cir
965	3	10.7	35	12	Q93206	Q93206 porcine cir
966	3	10.7	35	12	Q56131	Q56131 porcine cir
967	3	10.7	35	12	Q8B6X7	Q8b6x7 human rotav
968	3	10.7	35	13	Q9PU87	Q9pu87 catla catla
969	3	10.7	35	13	Q09132	Q09132 xenopus lae

970	3	10.7	35	13	Q09133	Q09133 xenopus lae
971	3	10.7	35	15	Q70411	Q70411 human immun
972	3	10.7	35	15	Q76748	Q76748 human immun
973	3	10.7	35	15	Q80458	Q80458 human immun
974	3	10.7	35	15	O91391	O91391 human immun
975	3	10.7	35	15	Q76728	Q76728 human immun
976	3	10.7	35	15	O40565	O40565 human immun
977	3	10.7	35	15	Q79885	Q79885 human immun
978	3	10.7	35	15	Q72954	Q72954 human immun
979	3	10.7	35	15	O71540	O71540 human immun
980	3	10.7	35	15	O40564	O40564 human immun
981	3	10.7	35	15	Q78812	Q78812 human immun
982	3	10.7	35	15	O71534	O71534 human immun
983	3	10.7	35	15	Q9QR10	Q9qr10 human immun
984	3	10.7	35	15	Q80457	Q80457 human immun
985	3	10.7	35	15	O40563	O40563 human immun
986	3	10.7	35	15	Q80609	Q80609 human immun
987	3	10.7	35	15	Q70215	Q70215 human immun
988	3	10.7	35	15	Q79494	Q79494 human immun
989	3	10.7	35	15	O91371	O91371 human immun
990	3	10.7	35	15	Q9IPY8	Q9ipy8 human immun
991	3	10.7	35	15	Q78049	Q78049 human immun
992	3	10.7	35	15	Q79477	Q79477 human immun
993	3	10.7	35	15	Q77703	Q77703 human immun
994	3	10.7	35	15	O91436	O91436 human immun
995	3	10.7	35	15	Q70322	Q70322 human immun
996	3	10.7	35	15	Q9IPX8	Q9ipx8 human immun
997	3	10.7	35	15	O91441	O91441 human immun
998	3	10.7	35	15	Q79478	Q79478 human immun
999	3	10.7	35	15	Q79481	Q79481 human immun
1000	3	10.7	35	15	Q79997	Q79997 human immun

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.

AC Q91Y90;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Parathyroid hormone (Fragment).

GN PTH.

OS Peromyscus maniculatus (Deer mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Peromyscus.

OX NCBI_TaxID=10042;

RN [1]

RP SEQUENCE FROM N.A.

RA Prince K.L., Dewey M.J.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF382953; AAK63072.1; -.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 17.9%; Score 5; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNLGK 7
|||||
Db 21 HNLGK 25

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 17.9%; Score 5; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNLGK 7
|||||
Db 21 HNLGK 25

RESULT 3

Q8KCG1

ID Q8KCG1 PRELIMINARY; PRT; 31 AA.
AC Q8KCG1;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein CT1460.
 GN CT1460.
 OS Chlorobium tepidum.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium.
 OX NCBI_TaxID=1097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;
 RX MEDLINE=22103685; PubMed=12093901;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
 RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
 RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
 RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
 RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
 RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of Chlorobium tepidum TLS, a
 RT photosynthetic, anaerobic, green-sulfur bacterium."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 DR EMBL; AE012903; AAM72688.1; -.
 DR TIGR; CT1460; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 31 AA; 3539 MW; 0353C55E1E8185CC CRC64;

Query Match 17.9%; Score 5; DB 16; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 LHHLI 22
 |||||
 Db 24 LHHLI 28

RESULT 4

Q8JAC6

ID Q8JAC6 PRELIMINARY; PRT; 35 AA.
 AC Q8JAC6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Gp120 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22068028; PubMed=12072500;
 RA Kijak G.H., Simon V., Balfe P., Vanderhoeven J., Pampuro S.E.,
 RA Zala C., Ochoa C., Cahn P., Markowitz M., Salomon H.;
 RT "Origin of Human Immunodeficiency Virus Type 1 Quasispecies Emerging
 RT after Antiretroviral Treatment Interruption in Patients with
 RT Therapeutic Failure.";

RL J. Virol. 76:7000-7009(2002).
 DR EMBL; AF470757; AAM74604.1; -.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1 1
 FT NON_TER 35 35
 SQ SEQUENCE 35 AA; 3734 MW; DE5E0E3DEC9BE2B0 CRC64;

Query Match 17.9%; Score 5; DB 15; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQ 10
 |||||
 Db 9 GKSIQ 13

RESULT 5

Q51595

ID Q51595 PRELIMINARY; PRT; 39 AA.
 AC Q51595;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Acetoin:DCPIP oxidoreductase alpha and beta subunits, lipoat synthase,
 DE dihydrolipoamide dehydrogenase and ferredoxin (AcoA,B,C,S, and L) genes
 DE (Fragment).
 OS Pelobacter carbinolicus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Pelobacteraceae; Pelobacter.
 OX NCBI_TaxID=19;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gra Bd 1;
 RA Oppermann F.B., Steinbuechel A.;
 RT "Identification and molecular characterization of the aco genes
 RT encoding the Pelobacter carbinolicus acetoin dehydrogenase enzyme
 RT system."
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L24124; AAA91874.1; -.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4256 MW; AE9D84F64CD1126A CRC64;

Query Match 17.9%; Score 5; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRRF 16
 |||||
 Db 22 LRRRF 26

RESULT 6

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.

AC Q8GZQ8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE SNF-1 related kinase (Fragment).
 GN BKIN12.
 OS Hordeum vulgare var. distichum (Two-rowed barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=112509;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Igri;
 RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;
 RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF448389; AAN76447.1; -.
 KW Kinase.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 14.3%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLGK 7
 ||||
 Db 18 NLGK 21

RESULT 7

Q67781

ID Q67781 PRELIMINARY; PRT; 28 AA.
 AC Q67781;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PTP (Fragment).
 GN PTP.
 OS Human adenovirus type 31.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC cat# VR-1109;
 RA Ma Y., Mathews M.B.;
 RT "The structure, function, and evolution of adenovirus VA RNA: a
 RT phylogenetic approach."
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U52568; AAB00302.1; -.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3282 MW; 6601C5E66A98ACF6 CRC64;

Query Match 14.3%; Score 4; DB 12; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SIQD 11
||||
Db 1 SIQD 4

RESULT 8

Q67780

ID Q67780 PRELIMINARY; PRT; 28 AA.
AC Q67780;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PTP (Fragment).
GN PTP.
OS Human adenovirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10528;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC cat# VR-1095;
RA Ma Y., Mathews M.B.;
RT "The structure, function, and evolution of adenovirus VA RNA: a
phylogenetic approach."
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U52567; AAB00300.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3301 MW; 921195F72E98B9FE CRC64;

Query Match 14.3%; Score 4; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SIQD 11
||||
Db 1 SIQD 4

RESULT 9

Q9R4S6

ID Q9R4S6 PRELIMINARY; PRT; 29 AA.
AC Q9R4S6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Oligopeptidase (Fragment).
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE.
RX MEDLINE=95168853; PubMed=7864624;
RA Makinen K.K., Makinen P.L., Loesche W.J., Syed S.A.;
RT "Purification and general properties of an oligopeptidase from
Treponema denticola ATCC 35405--a human oral spirochete.";

RL Arch. Biochem. Biophys. 316:689-698(1995).
SQ SEQUENCE 29 AA; 3484 MW; 2F614C2387CCF68C CRC64;

Query Match 14.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 IAEI 25
|||
Db 11 IAEI 14

RESULT 10

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.
AC Q96PP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).
GN SPINK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,
RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,
RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,
RA Uitto J., Hovnanian A., Richard G.;
RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with
RT Netherton syndrome - Implications for mutation detection and first
RT case of prenatal diagnosis.";
RL J. Invest. Dermatol. 0:0-0(2001).
DR EMBL; AF295783; AAK97140.1; -.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 14.3%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLGK 7
|||
Db 14 NLGK 17

RESULT 11

P82235

ID P82235 PRELIMINARY; PRT; 29 AA.
AC P82235;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Brevinin-2TD.

OS *Rana temporaria* (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; *Rana*.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RX MEDLINE=99266278; PubMed=10333736;
 RA Simmaco M., Mignogna G., Barra D.;
 RT "Antimicrobial peptides from amphibian skin: what do they tell us?";
 RL Biopolymers 47:435-450(1998).
 CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST REPRESENTATIVE
 CC GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL SPECIES.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: SKIN.
 CC -!- SIMILARITY: BELONGS THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Amphibian skin; Antibiotic.
 FT DISULFID 23 29 BY SIMILARITY.
 SQ SEQUENCE 29 AA; 3234 MW; DDF8F76F48F1273C CRC64;

Query Match 14.3%; Score 4; DB 13; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHNL 5
 ||||
 Db 18 LHNL 21

RESULT 12

Q8KYE4

ID Q8KYE4 PRELIMINARY; PRT; 30 AA.
 AC Q8KYE4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 GN BXB0050.
 OS *Bacillus anthracis*.
 OG Plasmid pXO2.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A2012;
 RX MEDLINE=22061436; PubMed=12004073;
 RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
 RA Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
 RA Keim P., Fraser C.M.;
 RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
 RT *Bacillus anthracis*.";
 RL Science 296:2028-2033(2002).
 DR EMBL; AE011191; AAM26208.1; -.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 30 AA; 3515 MW; B3352D9BB791AEDF CRC64;

Query Match 14.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSIQ 10
||||
Db 4 KSIQ 7

RESULT 13

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.
AC Q9JMV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Luciferase alpha-subunit (Fragment).
GN LUXA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RA Lotz W., Bauer T.;
RT "luxAB/kan-cassette for site-directed insertion mutagenesis and
RT bacterial transcription studies.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RA Olsson O., Koncz C., Szalay A.;
RT "The use of luxA gene of the bacterial luciferase operon as a reporter
RT gene.";
RL Mol. Gen. Genet. 215:1-9(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RX MEDLINE=92114868; PubMed=1685011;
RA Escher A., O'Kane D.J., Szalay A.;
RT "The beta subunit polypeptide of Vibrio harveyi luciferase determines
RT light emission at 42 degrees C.";
RL Mol. Gen. Genet. 230:385-393(1991).
DR EMBL; AJ249443; CAB96206.1; -.
DR HSSP; P07740; 1LUC.
DR InterPro; IPR002103; Bac_luciferase.
DR Pfam; PF00296; bac_luciferase; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 14.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLGK 7
||||

RESULT 14

Q32617

ID Q32617 PRELIMINARY; PRT; 30 AA.
AC Q32617;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF30.
OS *Marchantia polymorpha* (Liverwort).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;
OC Marchantiaceae; *Marchantia*.
OX NCBI_TaxID=3197;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
RA Ozeki H.;
RT "Chloroplast gene organization deduced from complete sequence of
RT liverwort *Marchantia polymorpha* chloroplast DNA.";
RL Nature 322:572-574(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84247325; PubMed=6739292;
RA Yamano Y., Ohyama K., Komano T.;
RT "Nucleotide sequences of chloroplast 5S ribosomal RNA from cell
RT suspension cultures of the liverworts *Marchantia polymorpha* and
RT *Jungermannia subulata*.";
RL Nucleic Acids Res. 12:4621-4624(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087956; PubMed=6393057;
RA Umesono K., Inokuchi H., Ohyama K., Ozeki H.;
RT "Nucleotide sequence of *Marchantia polymorpha* chloroplast DNA: a
RT region possibly encoding three tRNAs and three proteins including a
RT homologue of *E. coli* ribosomal protein S14.";
RL Nucleic Acids Res. 12:9551-9565(1984).
RN [4]
RP SEQUENCE FROM N.A.
RA Fukuzawa H., Uchida Y., Yamano Y., Ohyama K., Komano T.;
RT "Molecular cloning of promoters functional in *Escherichia coli* from
RT chloroplast DNA of a liverwort, *Marchantia polymorpha*.";
RL Agric. Biol. Chem. 49:2725-2731(1985).
RN [5]
RP SEQUENCE FROM N.A.
RA Yamano Y., Kohchi T., Fukuzawa H., Ohyama K., Komano T.;
RT "Nucleotide sequences of chloroplast 4.5 S ribosomal RNA from a leafy
RT liverwort, *Jungermannia subulata*, and a thalloid liverwort, *Marchantia*
RT *polymorpha*.";
RL FEBS Lett. 185:203-207(1985).
RN [6]
RP SEQUENCE FROM N.A.
RA Fukuzawa H., Kohchi T., Shirai H., Ohyama K., Umesono K., Inokuchi H.,

RA Ozeki H.;
 RT "Coding sequences for chloroplast ribosomal protein S12 from the
 RT liverwort, *Marchantia polymorpha*, are separated far apart on the
 RT different DNA strands.";
 RL FEBS Lett. 198:11-15(1986).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Fukuzawa H., Yoshida T., Kohchi T., Okumura T., Sawano Y., Ohyama K.;
 RT "Splicing of group II introns in mRNAs coding for cytochrome b6 and
 RT subunit IV in liverwort *Marchantia polymorpha* chloroplast genome: Exon
 RT specifying a region coding for two genes with the spacer region.";
 RL FEBS Lett. 220:61-66(1987).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89028845; PubMed=2846189;
 RA Kohchi T., Ogura Y., Umesono K., Yamada Y., Komano T., Ozeki H.,
 RA Ohyama K.;
 RT "Ordered processing and splicing in a polycistronic transcript in
 RT liverwort chloroplasts.";
 RL Curr. Genet. 14:147-154(1988).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89068687; PubMed=3199436;
 RA Fukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H.,
 RA Ozeki H., Ohyama K.;
 RT "Structure and organization of *Marchantia polymorpha* chloroplast
 RT genome. III. Gene organization of the large single copy region from
 RT *rbcL* to *trnI*(CAU).";
 RL J. Mol. Biol. 203:333-351(1988).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91212240; PubMed=1708498;
 RA Shimada H., Sugiura M.;
 RT "Fine structural features of the chloroplast genome: comparison of the
 RT sequenced chloroplast genomes.";
 RL Nucleic Acids Res. 19:983-995(1991).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89068685; PubMed=2462054;
 RA Ohyama K., Fukuzawa H., Kohchi T., Sano T., Sano S., Shirai H.,
 RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S.i., Inokuchi H.,
 RA Ozeki H.;
 RT "Structure and organization of *Marchantia polymorpha* Chloroplast
 RT genome. I. cloning and gene identification.";
 RL J. Mol. Biol. 203:281-298(1988).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89068686; PubMed=2974085;
 RA Umesono K., Inokuchi H., Shiki Y., Takeuchi M., Chang Z., Fukuzawa H.,
 RA Kohchi T., Shirai H., Ohyama K., Ozeki H.;
 RT "Structure and organization of *Marchantia polymorpha* chloroplast
 RT genome. II. gene organization of the large single copy region from
 RT *rps'12* to *atpB*.";
 RL J. Mol. Biol. 203:299-331(1988).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89068688; PubMed=3199437;

RA Kohchi T., Shirai H., Fukuzawa H., Sano T., Komano T., Umesono K.,
 RA Inokuchi H., Ozeki H., Ohyama K.;
 RT "Structure and organization of Marchantia polymorpha chloroplast
 RT genome. IV. inverted repeat and small single copy regions.";
 RL J. Mol. Biol. 203:353-372(1988).
 DR EMBL; X04465; CAA28070.1; -.
 KW Chloroplast.
 SQ SEQUENCE 30 AA; 3842 MW; 41C170779F249D58 CRC64;

Query Match 14.3%; Score 4; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RFFL 18
 ||||
 Db 24 RFFL 27

RESULT 15

Q8MXE8

ID Q8MXE8 PRELIMINARY; PRT; 31 AA.
 AC Q8MXE8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein K07A9.4.
 GN K07A9.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Davidson S., O'Neal D.;
 RT "The sequence of C. elegans cosmid K07A9.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF099924; AAM98005.1; -.
 DR WormPep; K07A9.4; CE31709.
 KW Hypothetical protein.
 SQ SEQUENCE 31 AA; 3720 MW; 147938913DC940ED CRC64;

Query Match 14.3%; Score 4; DB 5; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 FFLH 19
|||
Db 21 FFLH 24

RESULT 16

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.
AC Q9MS77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Photosystem I protein M.
GN PSAM.
OS Phacus acuminata.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.
OX NCBI_TaxID=130316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21080550; PubMed=11212923;
RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;
RT "Comparison of psbK operon organization and group III intron content
RT in chloroplast genomes of 12 Euglenoid species.";
RL Mol. Gen. Genet. 264:682-690(2001).
DR EMBL; AF241276; AAF82438.1; -.
KW Chloroplast.
SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 14.3%; Score 4; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLGK 7
|||
Db 24 NLGK 27

RESULT 17

Q9DFI7

ID Q9DFI7 PRELIMINARY; PRT; 31 AA.
AC Q9DFI7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Double-sex like protein Dmrt5 (Fragment).
OS Monopterus albus (swamp eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Synbranchidae; Monopterus.
OX NCBI_TaxID=43700;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;

RA Huang X., Zhou R.;
 RT "A conserved family of doublesex related genes from fish."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF272957; AAG18566.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 DR PROSITE; PS50809; DM_DOMAIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3633 MW; 33A2E9B0B118DE2D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
 ||||
 Db 24 LIAE 27

RESULT 18

Q9DEW2

ID Q9DEW2 PRELIMINARY; PRT; 31 AA.
 AC Q9DEW2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Doublesex-related protein Dmrt15 (Fragment).
 GN DMRT15.
 OS Coturnix coturnix (Common quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TaxID=9091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Ren L., Zhou R.;
 RT "Evolutionary conservation of doublesex-related gene family in
 RT amphibian, reptile and bird."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY005392; AAG15564.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 DR PROSITE; PS50809; DM_DOMAIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3593 MW; 211519B0B7B3D92D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
 ||||
 Db 24 LIAE 27

RESULT 19

Q9DFH7

ID Q9DFH7 PRELIMINARY; PRT; 31 AA.
 AC Q9DFH7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Doublesex-like protein Dmrt6 (Fragment).
 OS Mastacembelus aculeatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
 OC Mastacembelidae; Mastacembelus.
 OX NCBI_TaxID=138129;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou R.;
 RT "A conserved family of doublesex related genes from fish.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF272971; AAG18556.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 DR PROSITE; PS50809; DM_DOMAIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3653 MW; 211519B0A769B92D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
 ||||
 Db 24 LIAE 27

RESULT 20

Q9DFI2

ID Q9DFI2 PRELIMINARY; PRT; 31 AA.
 AC Q9DFI2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Doublesex-like protein Dmrt6 (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou R.;
 RT "A conserved family of doublesex related genes from fish.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF272962; AAG18558.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.

DR Pfam; PF00751; DM-domain; 1.
DR PROSITE; PS50809; DM_DOMAIN_2; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3653 MW; 211519B0A769B92D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
|||
Db 24 LIAE 27

RESULT 21

Q9DFH8

ID Q9DFH8 PRELIMINARY; PRT; 31 AA.
AC Q9DFH8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Doublesex-like protein Dmrt5 (Fragment).
OS Mastacembelus aculeatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Mastacembelidae; Mastacembelus.
OX NCBI_TaxID=138129;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang X., Zhou R.;
RT "A conserved family of doublesex related genes from fish."
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF272970; AAG18555.1; -.
DR InterPro; IPR001275; DM_DNA-binding.
DR Pfam; PF00751; DM-domain; 1.
DR PROSITE; PS50809; DM_DOMAIN_2; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3633 MW; 33A2E9B0B118DE2D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
|||
Db 24 LIAE 27

RESULT 22

Q9DFI6

ID Q9DFI6 PRELIMINARY; PRT; 31 AA.
AC Q9DFI6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Double-sex like protein Dmrt6 (Fragment).
 OS Monopterus albus (swamp eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
 OC Synbranchidae; Monopterus.
 OX NCBI_TaxID=43700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Huang X., Zhou R.;
 RT "A conserved family of doublesex related genes from fish."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF272958; AAG18567.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 DR PROSITE; PS50809; DM_DOMAIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3653 MW; 211519B0A769B92D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
 ||||
 Db 24 LIAE 27

RESULT 23

Q9DFI1
 ID Q9DFI1 PRELIMINARY; PRT; 31 AA.
 AC Q9DFI1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Doublesex-like protein Dmrt11 (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou R.;
 RT "A conserved family of doublesex related genes from fish."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF272963; AAG18559.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3734 MW; 211519BE4019B92D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
|||
Db 24 LIAE 27

RESULT 24

Q9DEW1

ID Q9DEW1 PRELIMINARY; PRT; 31 AA.
AC Q9DEW1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Doublesex-related protein Dmrt16 (Fragment).
GN DMRT16.
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Ren L., Zhou R.;
RT "Evolutionary conservation of doublesex-related gene family in
RT amphibian, reptile and bird.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY005393; AAG15565.1; -.
DR InterPro; IPR001275; DM_DNA-binding.
DR Pfam; PF00751; DM-domain; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3525 MW; 4FC922DE73F934FB CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
|||
Db 24 LIAE 27

RESULT 25

Q9DEW3

ID Q9DEW3 PRELIMINARY; PRT; 31 AA.
AC Q9DEW3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Doublesex-related protein Dmrt6 (Fragment).
GN DMRT6.
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Coturnix.
 OX NCBI_TaxID=9091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Ren L., Zhou R.;
 RT "Evolutionary conservation of doublesex-related gene family in
 RT amphibian, reptile and bird."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY005391; AAG15563.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 DR PROSITE; PS50809; DM_DOMAIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3653 MW; 211519B0A769B92D CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
 ||||
 Db 24 LIAE 27

RESULT 26

Q90Z24

ID Q90Z24 PRELIMINARY; PRT; 31 AA.
 AC Q90Z24;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Dmrt1 (Fragment).
 OS Monopterus albus (swamp eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
 OC Synbranchidae; Monopterus.
 OX NCBI_TaxID=43700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou R., Huang X.;
 RT "Molecular cloning and expression of rice field eel Dmrt1."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF378149; AAK59253.1; -.
 DR InterPro; IPR001275; DM_DNA-binding.
 DR Pfam; PF00751; DM-domain; 1.
 DR PROSITE; PS50809; DM_DOMAIN_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3753 MW; BB91FDB73A1F0ADD CRC64;

Query Match 14.3%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LIAE 24
|||
Db 24 LIAE 27

RESULT 27

Q8KEV8

ID Q8KEV8 PRELIMINARY; PRT; 31 AA.
AC Q8KEV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein CT0574.
GN CT0574.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouiri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012832; AAM71816.1; -.
DR TIGR; CT0574; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 31 AA; 3734 MW; 588CF6AC05DA440B CRC64;

Query Match 14.3%; Score 4; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LIAE 24
|||
Db 14 LIAE 17

RESULT 28

Q8KEV3

ID Q8KEV3 PRELIMINARY; PRT; 31 AA.
AC Q8KEV3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein CT0579.
GN CT0579.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;

OC Chlorobium.
 OX NCBI_TaxID=1097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;
 RX MEDLINE=22103685; PubMed=12093901;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
 RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
 RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
 RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
 RA Vamathevan J., Khouiri H., White O., Gruber T.M., Ketchum K.A.,
 RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of Chlorobium tepidum TLS, a
 RT photosynthetic, anaerobic, green-sulfur bacterium."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 DR EMBL; AE012832; AAM71821.1; -.
 DR TIGR; CT0579; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 31 AA; 3617 MW; 265C9621F2F40044 CRC64;

Query Match 14.3%; Score 4; DB 16; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 RRFF 17
 ||||
 Db 4 RRFF 7

RESULT 29

Q96Q53

ID Q96Q53 PRELIMINARY; PRT; 32 AA.
 AC Q96Q53;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mitochondrial ribosomal protein L17 (Fragment).
 GN MRPL17.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429115; PubMed=11543634;
 RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
 RA Watanabe K., Tanaka T.;
 RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
 RT to the chromosomes and implications for human disorders."
 RL Genomics 77:65-70(2001).
 DR EMBL; AB051620; BAB54948.1; -.
 KW Ribosomal protein.
 FT NON_TER 1 1
 SQ SEQUENCE 32 AA; 3542 MW; 1322815AE11A6404 CRC64;

Query Match 14.3%; Score 4; DB 4; Length 32;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QDLR 13
||||
Db 11 QDLR 14

RESULT 30

Q9DZ37

ID Q9DZ37 PRELIMINARY; PRT; 32 AA.
AC Q9DZ37;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Pol polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,
RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
RA Siliciano R., D'Aquila R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
RT infection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR EMBL; AF292795; AAG25401.1; -.
KW Polyprotein.
FT NON_TER 1 1
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3951 MW; B6AD13060D1EEA1A CRC64;

Query Match 14.3%; Score 4; DB 15; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RFFL 18
||||
Db 8 RFFL 11

RESULT 31

Q9P1T8

ID Q9P1T8 PRELIMINARY; PRT; 33 AA.
AC Q9P1T8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mutant chemokine receptor CCR5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99392755; PubMed=10465086;
 RA Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
 RA Bond V.C.;
 RT "Characterization of a third CCR5 amplicon from CCR5-delta32-
 RT heterozygous HIV-1-infected individuals.";
 RL AIDS 13:1585-1586(1999).
 DR EMBL; AF052244; AAF65577.1; -.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 33 AA; 3477 MW; 664294782E2DB3E1 CRC64;

Query Match 14.3%; Score 4; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGKS 8
 ||||
 Db 30 LGKS 33

RESULT 32

Q8N4J9

ID Q8N4J9 PRELIMINARY; PRT; 33 AA.
 AC Q8N4J9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC033964; AAH33964.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 33 AA; 3884 MW; 1A0E9E343070B4E1 CRC64;

Query Match 14.3%; Score 4; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLHN 4
 ||||
 Db 17 LLHN 20

RESULT 33

Q9AR83

ID Q9AR83 PRELIMINARY; PRT; 33 AA.

AC Q9AR83;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Putative metallothionein-like protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seedling aerial parts;
 RA Dubos C., Le Provost G., Salin F., Lalane C., Madur D., Frigerio J.M.,
 RA Plomion C.;
 RT "Identification and characterization of water-deficit responsive genes
 RT in Maritime pine (Pinus pinaster Ait.) seedlings.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ309103; CAC35976.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 33 AA; 3610 MW; A89612AE71CD728C CRC64;

 Query Match 14.3%; Score 4; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 HLIA 23
 ||||
 Db 3 HLIA 6

RESULT 34

Q9RI14

ID Q9RI14 PRELIMINARY; PRT; 33 AA.
 AC Q9RI14;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE YPCD1.70c protein (Fragment).
 GN YPCD1.70C.
 OS Yersinia pestis.
 OG Plasmid pCD1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis; PLASMID=pCD1;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
 RL Nature 413:523-527(2001).

DR EMBL; AL117189; CAB54947.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3882 MW; 69B9646EC9FF34DE CRC64;

Query Match 14.3%; Score 4; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 HLIA 23
|||
Db 30 HLIA 33

RESULT 35

Q9R5U1

ID Q9R5U1 PRELIMINARY; PRT; 34 AA.
AC Q9R5U1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PEB4=MAJOR antigenic peptide (Fragment).
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE.
RX MEDLINE=91358413; PubMed=1885571;
RA Pei Z.H., Ellison R.T.III., Blaser M.J.;
RT "Identification, purification, and characterization of major antigenic
RT proteins of Campylobacter jejuni."
RL J. Biol. Chem. 266:16363-16369(1991).
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3665 MW; 73BECEFA922507D2 CRC64;

Query Match 14.3%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSI 9
|||
Db 8 GKSI 11

RESULT 36

Q9RCC0

ID Q9RCC0 PRELIMINARY; PRT; 34 AA.
AC Q9RCC0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ferrochelatase (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme synthetase)
DE (Fragment).
GN HEMH.
OS Yersinia pseudotuberculosis (type O:1b).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=109458;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pa3606;
 RX MEDLINE=20392461; PubMed=10931327;
 RA Skurnik M., Peippo A., Ervela E.;
 RT "Characterization of the O-antigen gene clusters of Yersinia
 RT pseudotuberculosis and the cryptic O-antigen gene cluster of Yersinia
 RT pestis shows that the plague bacillus is most closely related to and
 RT has evolved from Y. pseudotuberculosis serotype O:1b.";
 RL Mol. Microbiol. 37:316-330(2000).
 CC -!- FUNCTION: CATALYZES THE FERROUS INSERTION INTO PROTOPORPHYRIN IX
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: PROTOPORPHYRIN + FE(2+) = PROTOHEME + 2 H(+).
 CC -!- PATHWAY: PROTOHEME BIOSYNTHESIS; LAST STEP.
 CC -!- SIMILARITY: BELONGS TO THE FERROCHELATASE FAMILY.
 DR EMBL; AJ251712; CAB63288.1; -.
 DR InterPro; IPR001015; Ferrochelatase.
 DR Pfam; PF00762; Ferrochelatase; 1.
 KW Heme biosynthesis; Iron; Lyase; Porphyrin biosynthesis.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3921 MW; 948552A9D80C2FE8 CRC64;

Query Match 14.3%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 FFLH 19
 ||||
 Db 1 FFLH 4

RESULT 37

Q9RCD1
 ID Q9RCD1 PRELIMINARY; PRT; 34 AA.
 AC Q9RCD1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ferrochelatase (EC 4.99.1.1) (Ferrochelatase) (Protoheme ferro-lyase)
 DE (Heme synthetase) (Fragment).
 GN HEMH.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EV76;
 RX MEDLINE=20392461; PubMed=10931327;
 RA Skurnik M., Peippo A., Ervela E.;
 RT "Characterization of the O-antigen gene clusters of Yersinia
 RT pseudotuberculosis and the cryptic O-antigen gene cluster of Yersinia
 RT pestis shows that the plague bacillus is most closely related to and
 RT has evolved from Y. pseudotuberculosis serotype O:1b.";

RL Mol. Microbiol. 37:316-330(2000).
 CC -!- FUNCTION: CATALYZES THE FERROUS INSERTION INTO PROTOPORPHYRIN IX
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: PROTOPORPHYRIN + FE(2+) = PROTOHEME + 2 H(+).
 CC -!- PATHWAY: PROTOHEME BIOSYNTHESIS; LAST STEP.
 CC -!- SIMILARITY: BELONGS TO THE FERROCHELATASE FAMILY.
 DR EMBL; AJ251713; CAB63269.1; -.
 DR InterPro; IPR001015; Ferrochelatase.
 DR Pfam; PF00762; Ferrochelatase; 1.
 KW Heme biosynthesis; Iron; Lyase; Porphyrin biosynthesis.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3921 MW; 948552A9D80C2FE8 CRC64;

Query Match 14.3%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 FFLH 19
 ||||
 Db 1 FFLH 4

RESULT 38

Q95LA4

ID Q95LA4 PRELIMINARY; PRT; 34 AA.
 AC Q95LA4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE LIM homeodomain protein 3b (Fragment).
 GN LHX3.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21453325; PubMed=11470784;
 RA Sloop K.W., Dwyer C.J., Rhodes S.J.;
 RT "An isoform-specific inhibitory domain regulates the Lhx3 lim
 RT homeodomain factor holoprotein and the production of a functional
 RT alternate translation form."
 RL J. Biol. Chem. 276:36311-36319(2001).
 DR EMBL; AF370449; AAL09574.1; -.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3674 MW; D7A2F1258F8E414A CRC64;

Query Match 14.3%; Score 4; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
 ||||
 Db 28 DLRR 31

RESULT 39

Q95LA6

ID Q95LA6 PRELIMINARY; PRT; 34 AA.
 AC Q95LA6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE LIM homeodomain protein 3b (Fragment).
 GN LHX3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21453325; PubMed=11470784;
 RA Sloop K.W., Dwyer C.J., Rhodes S.J.;
 RT "An isoform-specific inhibitory domain regulates the Lhx3 lim
 RT homeodomain factor holoprotein and the production of a functional
 RT alternate translation form."
 RL J. Biol. Chem. 276:36311-36319(2001).
 DR EMBL; AF370445; AAL09570.1; -.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3748 MW; 7083C3258F8E414C CRC64;

Query Match 14.3%; Score 4; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
 ||||
 Db 28 DLRR 31

RESULT 40

Q91ZX2

ID Q91ZX2 PRELIMINARY; PRT; 34 AA.
 AC Q91ZX2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE LIM homeodomain protein 3b (Fragment).
 GN LHX3.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21453325; PubMed=11470784;
 RA Sloop K.W., Dwyer C.J., Rhodes S.J.;
 RT "An isoform-specific inhibitory domain regulates the Lhx3 lim
 RT homeodomain factor holoprotein and the production of a functional
 RT alternate translation form."
 RL J. Biol. Chem. 276:36311-36319(2001).

DR EMBL; AF370450; AAL09575.1; -.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3746 MW; D7A2F215BC88212C CRC64;

Query Match 14.3%; Score 4; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
|||
Db 28 DLRR 31

Search completed: January 14, 2004, 10:42:13
Job time : 33.9346 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 4.62305 Seconds
 (without alignments)
 284.822 Million cell updates/sec

Title: US-09-843-221A-169
 Perfect score: 28
 Sequence: 1 LLHNLGKSIQDLRRRFFLHHLIAEIHITA 28

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	17.9	36	1	ELH_THETS	P80594 theromyzon
2	4	14.3	31	1	PSAM_EUGGR	P31479 euglena gra
3	4	14.3	34	1	DEF7_RABIT	P80223 oryctolagus
4	4	14.3	36	1	PAHO_MACMU	P33684 macaca mula
5	4	14.3	36	1	PAHO_RABIT	P41336 oryctolagus
6	4	14.3	36	1	Y4KD_BPCHP	P19188 bacterioph
7	3	10.7	28	1	FIBA_CANFA	P02673 canis famil
8	3	10.7	28	1	GTS5_CHICK	P20137 gallus gall
9	3	10.7	28	1	HSP4_OCTVU	P83216 octopus vul
10	3	10.7	28	1	PA23_TRIST	P82894 trimeresuru
11	3	10.7	28	1	VG9_SPV4	P11341 spiroplasma
12	3	10.7	28	1	VI03_VACCP	Q00334 vaccinia vi
13	3	10.7	28	1	Y073_ARCFU	O30163 archaeoglob
14	3	10.7	28	1	YA79_ARCFU	O29184 archaeoglob
15	3	10.7	29	1	12AH_CLOS4	P21215 clostridium
16	3	10.7	29	1	DMS5_PHYSA	P80281 phyllomedus
17	3	10.7	29	1	P2SM_LOXIN	P83046 loxosceles

18	3	10.7	29	1	PRO1_DACGL	P18689	dactylis gl
19	3	10.7	30	1	CH60_CLOPA	P81339	clostridium
20	3	10.7	30	1	HSP5_OCTVU	P83217	octopus vul
21	3	10.7	30	1	MMAL_DERMI	P16312	dermatophag
22	3	10.7	30	1	NUO2_SOLTU	P80268	solanum tub
23	3	10.7	30	1	PRT1_CLUPA	P02335	clupea pall
24	3	10.7	30	1	PRT2_ONCMY	P02331	oncorhynchu
25	3	10.7	30	1	PRT3_ONCMY	P02332	oncorhynchu
26	3	10.7	30	1	PRT4_ONCMY	P02333	oncorhynchu
27	3	10.7	30	1	PRTB_ONCMY	P12819	oncorhynchu
28	3	10.7	30	1	PSAM_ODOSI	P49487	odontella s
29	3	10.7	30	1	PSAM_PINTH	P41601	pinus thunb
30	3	10.7	30	1	PSAM_PORPU	P51395	porphyra pu
31	3	10.7	30	1	RL18_HALCU	P05970	halobacteri
32	3	10.7	31	1	COX4_NEUCR	P06809	neurospora
33	3	10.7	31	1	DEJP_DROME	P81160	drosophila
34	3	10.7	31	1	GP37_BPSP1	O48393	bacterioph
35	3	10.7	31	1	NAP4_HUMAN	P19877	homo sapien
36	3	10.7	31	1	PETL_ODOSI	P49524	odontella s
37	3	10.7	31	1	PRT2_CLUPA	P02336	clupea pall
38	3	10.7	31	1	PRT3_CLUPA	P02337	clupea pall
39	3	10.7	31	1	SCK5_ANDMA	P31719	androctonus
40	3	10.7	31	1	SCKL_LEIQH	P16341	leiurus qui
41	3	10.7	31	1	TXA3_PARAC	P09949	parasicyoni
42	3	10.7	31	1	Y3KD_BPCHP	P19187	bacterioph
43	3	10.7	32	1	CAL2_ONCKE	P01264	oncorhynchu
44	3	10.7	32	1	CAL3_ONCKI	P01265	oncorhynchu
45	3	10.7	32	1	CAL_ANGJA	P01262	anguilla ja
46	3	10.7	32	1	CAR1_ECHCA	Q9prp9	echis carin
47	3	10.7	32	1	ERH_PIG	P80230	sus scrofa
48	3	10.7	32	1	FLA1_METHU	P17603	methanospir
49	3	10.7	32	1	IAPP_PIG	Q29119	sus scrofa
50	3	10.7	32	1	MIFH_TRITR	P81748	trichuris t
51	3	10.7	32	1	P1SM_LOXIN	P83045	loxosceles
52	3	10.7	32	1	PRI3_ONCMY	P02330	oncorhynchu
53	3	10.7	32	1	PRT1_ESOLU	P02325	esox lucius
54	3	10.7	32	1	PRT1_ONCKE	P02327	oncorhynchu
55	3	10.7	32	1	PRT5_ONCMY	P02334	oncorhynchu
56	3	10.7	32	1	PRT6_ONCMY	P08145	oncorhynchu
57	3	10.7	32	1	PRT7_ONCMY	P08146	oncorhynchu
58	3	10.7	32	1	PRT8_ONCMY	P12817	oncorhynchu
59	3	10.7	32	1	PRT9_ONCMY	P08147	oncorhynchu
60	3	10.7	32	1	PRTA_ONCMY	P12818	oncorhynchu
61	3	10.7	32	1	PRT_ORYLA	Q91185	oryzias lat
62	3	10.7	32	1	PSAM_MARPO	P31590	marchantia
63	3	10.7	32	1	UC09_MAIZE	P80615	zea mays (m
64	3	10.7	32	1	Y160_BPT4	P39247	bacterioph
65	3	10.7	32	1	YH17_HAEIN	P44295	haemophilus
66	3	10.7	33	1	COA2_BPI22	P15414	bacterioph
67	3	10.7	33	1	COA2_BPIKE	P03678	bacterioph
68	3	10.7	33	1	DEF1_MESAU	P81465	mesocricetu
69	3	10.7	33	1	DEF3_MESAU	P81467	mesocricetu
70	3	10.7	33	1	GAST_DIDMA	P33713	didelphis m
71	3	10.7	33	1	GGN1_RANRU	P80395	rana rugosa
72	3	10.7	33	1	MBP1_MAIZE	P28794	zea mays (m
73	3	10.7	33	1	OREX_BOVIN	P56717	bos taurus
74	3	10.7	33	1	PRI1_ONCMY	P02326	oncorhynchu

75	3	10.7	33	1	PRI2_ONCMY	P02328	oncorhynchu
76	3	10.7	33	1	PRTB_MUGCE	P08130	mugil cepha
77	3	10.7	33	1	RUGB_RANRU	P80955	rana rugosa
78	3	10.7	33	1	SCX9_BUTOC	P04099	buthus occi
79	3	10.7	33	1	Y474_BORBU	O51430	borrelia bu
80	3	10.7	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
81	3	10.7	33	1	YLCH_BP82	Q37869	bacterioph
82	3	10.7	34	1	BUTH_ANDAU	P56685	androctonus
83	3	10.7	34	1	EF2_RABIT	P55823	oryctolagus
84	3	10.7	34	1	PRT1_SAROR	P25327	sarda orien
85	3	10.7	34	1	PRT1_SCOSC	P83264	scomber sco
86	3	10.7	34	1	PRT1_THUTH	P02321	thunnus thy
87	3	10.7	34	1	PRT2_SCOSC	P83265	scomber sco
88	3	10.7	34	1	PRT2_THUTH	P02322	thunnus thy
89	3	10.7	34	1	PRT_DICLA	Q9ps27	dicentrarch
90	3	10.7	34	1	PRT_PERFV	P29629	perca flave
91	3	10.7	34	1	PSAI_SOYBN	P49159	glycine max
92	3	10.7	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
93	3	10.7	34	1	RR2_OCHNE	Q40606	ochrosphaer
94	3	10.7	34	1	YC12_GUITH	O78460	guillardia
95	3	10.7	34	1	YC12_ODOSI	P49529	odontella s
96	3	10.7	35	1	CECA_AEDAL	P81417	aedes albop
97	3	10.7	35	1	COPA_CANFA	P40765	canis famil
98	3	10.7	35	1	DEFB_MYTED	P81611	mytilus edu
99	3	10.7	35	1	END4_YEREN	P42691	yersinia en
100	3	10.7	35	1	FLAV_NOSSM	P35707	nostoc sp.
101	3	10.7	35	1	NP30_STAAU	P21222	staphylococ
102	3	10.7	35	1	PSBM_SYNY3	P72701	synechocyst
103	3	10.7	35	1	Y644_ARCFU	O29613	archaeoglob
104	3	10.7	35	1	YQB5_CAEEL	Q09258	caenorhabdi
105	3	10.7	36	1	NIFH_ENTAG	P26249	enterobacte
106	3	10.7	36	1	PAHO_ANSAN	P06304	anser anser
107	3	10.7	36	1	PAHO_CERSI	P37999	ceratotheri
108	3	10.7	36	1	PAHO_DIDMA	P18107	didelphis m
109	3	10.7	36	1	PAHO_EQUZE	P38000	equus zebra
110	3	10.7	36	1	PAHO_ERIEU	P41335	erinaceus e
111	3	10.7	36	1	PAHO_TAPPI	P39659	tapirus pin
112	3	10.7	36	1	PSAI_BRAOL	Q31909	brassica ol
113	3	10.7	36	1	PSAI_SKECO	O96813	skeletonema
114	3	10.7	36	1	PSAI_TOBAC	P12187	nicotiana t
115	3	10.7	36	1	PSBM_SYNEL	Q8dha7	synechococc
116	3	10.7	36	1	Y297_ARCFU	O29945	archaeoglob
117	3	10.7	36	1	Y609_BORBU	O51554	borrelia bu
118	3	10.7	36	1	Y619_ARCFU	O29636	archaeoglob
119	3	10.7	37	1	DEF4_ANDAU	P56686	androctonus
120	3	10.7	37	1	DEFA_MYTED	P81610	mytilus edu
121	3	10.7	37	1	ES2A_RANES	P40845	rana escule
122	3	10.7	37	1	ES2B_RANES	P40846	rana escule
123	3	10.7	37	1	IAPP_CRIGR	P19890	cricetulus
124	3	10.7	37	1	OGT1_RABIT	P81436	oryctolagus
125	3	10.7	37	1	OP2B_OXYKI	P83249	oxyopes kit
126	3	10.7	37	1	POLN_WEEV	P13896	western equ
127	3	10.7	37	1	PRT3_SCYCA	P30258	scyliorhinu
128	3	10.7	37	1	PSAI_ARATH	P56768	arabidopsis
129	3	10.7	37	1	PSAJ_EUGGR	P30394	euglena gra
130	3	10.7	37	1	REV_SIVM2	P08809	simian immu
131	3	10.7	37	1	RK36_ARATH	P12144	arabidopsis

132	3	10.7	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
133	3	10.7	37	1	RK36_EPIVI	P30069	epifagus vi
134	3	10.7	37	1	RK36_LOTJA	Q9bbq2	lotus japon
135	3	10.7	37	1	RK36_MARPO	P12142	marchantia
136	3	10.7	37	1	RK36_OENHO	Q9mtj1	oenothera h
137	3	10.7	37	1	RK36_ORYSA	P12143	oryza sativ
138	3	10.7	37	1	RK36_PEA	P07815	pisum sativ
139	3	10.7	37	1	RK36_PINTH	P41631	pinus thunb
140	3	10.7	37	1	RK36_PSINU	Q8why9	psilotum nu
141	3	10.7	37	1	RK36_SPIOL	P12230	spinacia ol
142	3	10.7	37	1	RL36_ANASP	Q8ypk0	anabaena sp
143	3	10.7	37	1	RL36_BACST	P07841	bacillus st
144	3	10.7	37	1	RL36_NEIMA	Q9jrb2	neisseria m
145	3	10.7	37	1	RL7_CLOPA	P05393	clostridium
146	3	10.7	37	1	SCK2_LEIQH	P45628	leiurus qui
147	3	10.7	37	1	SCKC_LEIQH	P13487	leiurus qui
148	3	10.7	37	1	VG65_BPPH2	P16515	bacterioph
149	3	10.7	37	1	VG65_BPPZA	P08384	bacterioph
150	3	10.7	38	1	CRS3_NOTGO	P15534	nototodarus
151	3	10.7	38	1	DEF4_LEIQH	P41965	leiurus qui
152	3	10.7	38	1	DEF1_MYTGA	P80571	mytilus gal
153	3	10.7	38	1	DNP_DENAN	P28374	dendroaspis
154	3	10.7	38	1	MFA2_USTMA	P31963	ustilago ma
155	3	10.7	38	1	PSBF_TOBAC	P05171	nicotiana t
156	3	10.7	38	1	PSBM_CYAPA	P48107	cyanophora
157	3	10.7	38	1	RL36_SYNY3	P73300	synechocyst
158	3	10.7	38	1	VCOM_BPD10	Q38200	bacterioph
159	3	10.7	38	1	VG8_SPV4	P11340	spiroplasma
160	3	10.7	38	1	YF07_HAEIN	P44229	haemophilus
161	3	10.7	39	1	ARME_BOVIN	P80513	bos taurus
162	3	10.7	39	1	COA2_BPPM2	P15794	bacterioph
163	3	10.7	39	1	PA2_AGKBI	Q9psf9	agkistrodon
164	3	10.7	39	1	PRT1_BUFJA	P24641	bufo japoni
165	3	10.7	39	1	PRT2_BUFJA	P24642	bufo japoni
166	3	10.7	39	1	PSBF_GNEGN	Q9gfc3	gnetum gnem
167	3	10.7	39	1	PSBF_MARPO	P06853	marchantia
168	3	10.7	39	1	PSBF_ORYSA	P12088	oryza sativ
169	3	10.7	39	1	PSBF_PINTH	P41616	pinus thunb
170	3	10.7	39	1	PSBF_PSINU	Q8wi05	psilotum nu
171	3	10.7	39	1	PSBY_SYNY3	P73676	synechocyst
172	3	10.7	39	1	Y410_BORBU	O51371	borrelia bu
173	3	10.7	40	1	ALB1_TRASC	P81188	trachemys s
174	3	10.7	40	1	ASPG_RAT	P30919	rattus norv
175	3	10.7	40	1	CSP2_STRMT	O33666	streptococc
176	3	10.7	40	1	CSP3_STRMT	O33668	streptococc
177	3	10.7	40	1	GKBL_GINBI	P83171	ginkgo bilo
178	3	10.7	40	1	H2B3_ECHES	P13283	echinus esc
179	3	10.7	40	1	HPT_RABIT	P19007	oryctolagus
180	3	10.7	40	1	HS9A_RABIT	P30946	oryctolagus
181	3	10.7	40	1	ITAV_BOVIN	P80746	bos taurus
182	3	10.7	40	1	LHB1_ECTHL	P80106	ectothiorho
183	3	10.7	40	1	PHAC_MASLA	P11389	mastigoclad
184	3	10.7	40	1	PRE_BACLI	P18189	bacillus li
185	3	10.7	40	1	PSAI_PEA	P17227	pisum sativ
186	3	10.7	40	1	PSAJ_CYAPA	P48117	cyanophora
187	3	10.7	40	1	R18C_BOVIN	P82917	bos taurus
188	3	10.7	40	1	R362_STRCO	Q93jh3	streptomyce

189	3	10.7	40	1	RK33_PEA	P51416	pisum sativ
190	3	10.7	40	1	RL36_CORGL	Q8nmn8	corynebacte
191	3	10.7	40	1	UC11_MAIZE	P80617	zea mays (m
192	3	10.7	40	1	UC12_MAIZE	P80618	zea mays (m
193	2	7.1	28	1	ACON_CANAL	P82611	candida alb
194	2	7.1	28	1	APC1_RABIT	P33047	oryctolagus
195	2	7.1	28	1	ARYA_PSEPU	P35902	pseudomonas
196	2	7.1	28	1	ARYC_NOCGL	P80008	nocardia gl
197	2	7.1	28	1	C1QC_RAT	P31722	rattus norv
198	2	7.1	28	1	CH60_MYCSM	P80673	mycobacteri
199	2	7.1	28	1	COXB_SOLTU	P80499	solanum tub
200	2	7.1	28	1	ETX2_BACCE	P80568	bacillus ce
201	2	7.1	28	1	FLA1_TREPH	P21988	treponema p
202	2	7.1	28	1	GRP_ALLMI	P31886	alligator m
203	2	7.1	28	1	GUN_SCHCO	P81190	schizophyll
204	2	7.1	28	1	GVPC_OSCAG	P80999	oscillatori
205	2	7.1	28	1	ICPP_VIPLE	P82475	vipera lebe
206	2	7.1	28	1	IEL1_MOMCH	P10296	momordica c
207	2	7.1	28	1	ITR3_LUFCY	P35628	luffa cylin
208	2	7.1	28	1	LECA_IRIHO	P36230	iris hollan
209	2	7.1	28	1	LPFS_ECOLI	P22183	escherichia
210	2	7.1	28	1	LPL_ECOLI	P09149	escherichia
211	2	7.1	28	1	LPL_SALTI	Q8z9h9	salmonella
212	2	7.1	28	1	LPL_SALTY	P03062	salmonella
213	2	7.1	28	1	LPW_SERMA	P03055	serratia ma
214	2	7.1	28	1	MAAI_RAT	P57113	rattus norv
215	2	7.1	28	1	MCDP_MEGPE	P04567	megabombus
216	2	7.1	28	1	MT2_BRANA	Q96353	brassica na
217	2	7.1	28	1	NLT2_WHEAT	P39085	triticum ae
218	2	7.1	28	1	OBP1_HYSCR	P81647	hystrix cri
219	2	7.1	28	1	OMPA_YERPS	P38399	yersinia ps
220	2	7.1	28	1	ORND_PLAOR	P25513	placobdella
221	2	7.1	28	1	OST1_CHICK	P80896	gallus gall
222	2	7.1	28	1	PA22_MICNI	P21791	micrurus ni
223	2	7.1	28	1	PA23_MICNI	P21792	micrurus ni
224	2	7.1	28	1	PA2C_PSEPO	P20260	pseudechis
225	2	7.1	28	1	PETL_CYAPA	P48102	cyanophora
226	2	7.1	28	1	PHR_METTM	P58818	methanobact
227	2	7.1	28	1	PHYB_ASPFI	P81440	aspergillus
228	2	7.1	28	1	PP71_HCMVT	P24429	human cytom
229	2	7.1	28	1	PPOX_BOVIN	P56602	bos taurus
230	2	7.1	28	1	RIP_PLETU	P83245	pleurotus t
231	2	7.1	28	1	RS19_PHYS1	O66093	phytoplasma
232	2	7.1	28	1	SCX2_BUTSI	P15230	buthus sind
233	2	7.1	28	1	SLP1_LEIQH	P80669	leiurus qui
234	2	7.1	28	1	SMS2_ORENI	P81029	oreochromis
235	2	7.1	28	1	TXO2_AGEAP	P15971	agelenopsis
236	2	7.1	28	1	VAO_PLEOS	P21800	pleurotus o
237	2	7.1	28	1	VIP_ALLMI	P48142	alligator m
238	2	7.1	28	1	VIP_DIDMA	P39089	didelphis m
239	2	7.1	28	1	VIP_RANRI	P81016	rana ridibu
240	2	7.1	28	1	VIP_SCYCA	P09685	scyliorhinu
241	2	7.1	28	1	VIP_SHEEP	P04565	ovis aries
242	2	7.1	28	1	Y16P_BPT4	P39248	bacteriopho
243	2	7.1	29	1	28KD_TRIFO	P33405	tritrichomo
244	2	7.1	29	1	AMEL_RABIT	P12761	oryctolagus
245	2	7.1	29	1	ATP9_PICPJ	Q06838	pichia pijp

246	2	7.1	29	1	ATPA_BRYMA	P26965	bryopsis ma
247	2	7.1	29	1	BR2D_RANES	P40840	rana escule
248	2	7.1	29	1	BREE_RANES	P40841	rana escule
249	2	7.1	29	1	CERB_CERCA	P36191	ceratitidis c
250	2	7.1	29	1	COA1_BPI22	P15413	bacterioph
251	2	7.1	29	1	COXK_SHEEP	Q9tr28	ovis aries
252	2	7.1	29	1	CU36_LOCFI	P11737	locusta mig
253	2	7.1	29	1	CXO7_CONGE	P05483	conus geogr
254	2	7.1	29	1	CXOC_CONMA	P37300	conus magus
255	2	7.1	29	1	CXST_CONGE	P58844	conus geogr
256	2	7.1	29	1	DMD_RAT	P11530	rattus norv
257	2	7.1	29	1	GALA_ALLMI	P47215	alligator m
258	2	7.1	29	1	GALA_AMICA	P47214	amia calva
259	2	7.1	29	1	GALA_CHICK	P30802	gallus gall
260	2	7.1	29	1	GALA_ONCMY	P47213	oncorhynch
261	2	7.1	29	1	GALA_RANRI	P47216	rana ridibu
262	2	7.1	29	1	GALA_SHEEP	P31234	ovis aries
263	2	7.1	29	1	GLUC_ANAPL	P01276	anas platyr
264	2	7.1	29	1	GLUC_CALMI	P13189	callorhynch
265	2	7.1	29	1	GLUC_CHIBR	P31297	chinchilla
266	2	7.1	29	1	GLUC_DIDMA	P18108	didelphis m
267	2	7.1	29	1	GLUC_PLAFE	P23062	platichthys
268	2	7.1	29	1	GLUC_RABIT	P25449	oryctolagus
269	2	7.1	29	1	GLUC_TORMA	P09567	torpedo mar
270	2	7.1	29	1	H2B2_ECHES	P13282	echinus esc
271	2	7.1	29	1	HOXY_RHOOP	P22660	rhodococcus
272	2	7.1	29	1	HRJ_BOTJA	P20416	bothrops ja
273	2	7.1	29	1	HS98_NEUCR	P31540	neurospora
274	2	7.1	29	1	IPYR_DESVH	P19371	desulfovibr
275	2	7.1	29	1	ITH3_BOVIN	P56652	bos taurus
276	2	7.1	29	1	ITR1_CUCMA	P01074	cucurbita m
277	2	7.1	29	1	ITR1_LUFCY	P25849	luffa cylin
278	2	7.1	29	1	KDPF_ECOLI	P36937	escherichia
279	2	7.1	29	1	MDH_BURPS	P80536	burkholderi
280	2	7.1	29	1	MULR_ECHML	P81798	echis multi
281	2	7.1	29	1	NUO1_SOLTU	P80267	solanum tub
282	2	7.1	29	1	PCG4_PACGO	P82417	pachycondyl
283	2	7.1	29	1	PETN_ANASP	Q913p6	anabaena sp
284	2	7.1	29	1	PETN_CHAGL	Q8ma13	chaetosphae
285	2	7.1	29	1	PETN_CYAPA	P48258	cyanophora
286	2	7.1	29	1	PETN_GUIITH	O78498	guillardia
287	2	7.1	29	1	PETN_MARPO	P12177	marchantia
288	2	7.1	29	1	PETN_MESVI	Q9mus4	mesostigma
289	2	7.1	29	1	PETN_ODOSI	P49527	odontella s
290	2	7.1	29	1	PETN_PORPU	P51276	porphyra pu
291	2	7.1	29	1	PETN_PSINU	Q8wi23	psilotum nu
292	2	7.1	29	1	PETN_SKECO	O96807	skeletonema
293	2	7.1	29	1	PETN_SYNEL	Q8dkn2	synechococc
294	2	7.1	29	1	PETN_SYNY3	P72717	synechocyst
295	2	7.1	29	1	PK4_DICDI	P34103	dictyosteli
296	2	7.1	29	1	PSAF_SYNP6	P31083	synechococc
297	2	7.1	29	1	PSAK_SPIOL	P14627	spinacia ol
298	2	7.1	29	1	PSAM_GUIITH	O78448	guillardia
299	2	7.1	29	1	PSAX_SYNVU	P23320	synechococc
300	2	7.1	29	1	PSBI_SYNVU	P12240	synechococc
301	2	7.1	29	1	RL15_HALCU	P05971	halobacteri
302	2	7.1	29	1	RL15_STRLI	P49975	streptomyce

303	2	7.1	29	1	RP54_CLOKL	P38944	clostridium
304	2	7.1	29	1	RS7_METTE	O93639	methanosarc
305	2	7.1	29	1	SDHB_CLOPR	P80213	clostridium
306	2	7.1	29	1	TL16_SPIOL	P81834	spinacia ol
307	2	7.1	29	1	TLP_ACTDE	P81370	actinidia d
308	2	7.1	29	1	VARF_VIOAR	P58451	viola arven
309	2	7.1	29	1	Y15_BPT7	P03792	bacterioph
310	2	7.1	29	1	Y51_BPT3	P20326	bacterioph
311	2	7.1	29	1	YCX4_ODOSI	P49830	odontella s
312	2	7.1	29	1	YCX4_ODOSI	P49838	odontella s
313	2	7.1	30	1	2ENR_CLOTY	P11887	clostridium
314	2	7.1	30	1	ALAT_CHIVI	P38026	chinchilla
315	2	7.1	30	1	AATC_RABIT	P12343	oryctolagus
316	2	7.1	30	1	AATM_RABIT	P12345	oryctolagus
317	2	7.1	30	1	ACB1_DIGLA	P81624	digitalis l
318	2	7.1	30	1	ANF_RANRI	P09196	rana ridibu
319	2	7.1	30	1	CALM_LYTPI	P05935	lytechinus
320	2	7.1	30	1	CBAL_BACST	P13722	bacillus st
321	2	7.1	30	1	CIRA_CHAPA	P56871	chassalia p
322	2	7.1	30	1	CLPA_PINPS	P81671	pinus pinas
323	2	7.1	30	1	COAE_CORAM	P58101	corynebacte
324	2	7.1	30	1	COXC_SOLTU	P80500	solanum tub
325	2	7.1	30	1	CRG2_SCOWA	P19865	scoliodon w
326	2	7.1	30	1	CX2A_CONBE	P58625	conus betul
327	2	7.1	30	1	CX7A_CONTU	P58923	conus tulip
328	2	7.1	30	1	CXK4_CONST	P58921	conus stria
329	2	7.1	30	1	CXOB_CONPE	P56713	conus penna
330	2	7.1	30	1	CXVB_CONER	P58783	conus ermin
331	2	7.1	30	1	CY35_DESAC	P81079	desulfuromo
332	2	7.1	30	1	CYH1_VIOHE	P58433	viola heder
333	2	7.1	30	1	CY01_VIOOD	P82230	viola odora
334	2	7.1	30	1	CY02_VIOOD	P58434	viola odora
335	2	7.1	30	1	CY03_VIOOD	P58435	viola odora
336	2	7.1	30	1	CY07_VIOOD	P58439	viola odora
337	2	7.1	30	1	CY08_VIOOD	P58440	viola odora
338	2	7.1	30	1	CY09_VIOOD	P58441	viola odora
339	2	7.1	30	1	CY0A_VIOOD	P58442	viola odora
340	2	7.1	30	1	DEF2_MACMU	P82317	macaca mula
341	2	7.1	30	1	DIDH_COMTE	P80702	comamonas t
342	2	7.1	30	1	DIU2_HYLLI	P82015	hyles linea
343	2	7.1	30	1	DIU2_MANSE	P24858	manduca sex
344	2	7.1	30	1	DMS3_PHYSA	P80279	phyllomedus
345	2	7.1	30	1	END2_ONCKE	P01205	oncorhynch
346	2	7.1	30	1	FIBR_PANIN	P22775	panulirus i
347	2	7.1	30	1	FMBB_BACNO	P17829	bacteroides
348	2	7.1	30	1	FTN_BACFR	P28733	bacteroides
349	2	7.1	30	1	GLUM_ANGAN	P41521	anguilla an
350	2	7.1	30	1	HCY2_HOMAM	P82297	homarus ame
351	2	7.1	30	1	HETA_RADMA	P58691	radianthus
352	2	7.1	30	1	HYPH_HYBPA	P58445	hybanthus p
353	2	7.1	30	1	IHFB_RHILE	P80606	rhizobium l
354	2	7.1	30	1	ITI1_LAGLE	P26771	lagenaria l
355	2	7.1	30	1	ITR1_CITLA	P11969	citrullus l
356	2	7.1	30	1	ITR1_MOMCH	P10294	momordica c
357	2	7.1	30	1	ITR2_ECBEL	P12071	ecballium e
358	2	7.1	30	1	ITR2_LUFYC	P25850	luffa cylin
359	2	7.1	30	1	ITR3_CUCMC	P32041	cucumis mel

360	2	7.1	30	1	ITR3_MOMCO	P82410	momordica c
361	2	7.1	30	1	ITR6_CYCPE	P83397	cyclanthera
362	2	7.1	30	1	ITR7_CYCPE	P83398	cyclanthera
363	2	7.1	30	1	LAS1_PIG	P80171	sus scrofa
364	2	7.1	30	1	LEAH_PHAVU	P81870	phaseolus v
365	2	7.1	30	1	MDH_HELGE	P80037	heliobacter
366	2	7.1	30	1	NU5M_PISOC	P24999	pisaster oc
367	2	7.1	30	1	OTCC_AERPU	P11726	aeromonas p
368	2	7.1	30	1	P2CO_ARTSP	P37365	arthrobacte
369	2	7.1	30	1	PCCA_MYXXA	P81185	myxococcus
370	2	7.1	30	1	PCG2_PACGO	P82415	pachycondyl
371	2	7.1	30	1	PCG3_PACGO	P82416	pachycondyl
372	2	7.1	30	1	PCG5_PACGO	P82418	pachycondyl
373	2	7.1	30	1	PETN_NEPOL	Q9t101	nephroselmi
374	2	7.1	30	1	PLF4_RABIT	P83470	oryctolagus
375	2	7.1	30	1	PLMS_SQUAC	P82542	squalus aca
376	2	7.1	30	1	PMGY_CANAL	P82612	candida alb
377	2	7.1	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
378	2	7.1	30	1	PSAM_MESVI	Q9mus2	mesostigma
379	2	7.1	30	1	PYSD_METBA	P80524	methanosarc
380	2	7.1	30	1	RIPS_MOMCO	P20655	momordica c
381	2	7.1	30	1	RKGG_LEPKE	P21587	lepidochely
382	2	7.1	30	1	RNP_ODOVI	P19640	odocoileus
383	2	7.1	30	1	SCK2_TITSE	P08816	tityus serr
384	2	7.1	30	1	SCX2_CENLI	P18927	centruroides
385	2	7.1	30	1	SDHA_CLOPR	P80212	clostridium
386	2	7.1	30	1	TL1X_SPIOL	P82537	spinacia ol
387	2	7.1	30	1	TL29_SPIOL	P81833	spinacia ol
388	2	7.1	30	1	TX2_HETVE	P58426	heteropoda
389	2	7.1	30	1	UC35_MAIZE	P80641	zea mays (m
390	2	7.1	30	1	UDDP_SULAC	P80143	sulfolobus
391	2	7.1	30	1	UP61_UPEIN	P82037	uperoleia i
392	2	7.1	30	1	UP62_UPEIN	P82038	uperoleia i
393	2	7.1	30	1	URE1_ECOLI	Q03284	escherichia
394	2	7.1	30	1	VAA1_EQUAR	Q04236	equisetum a
395	2	7.1	30	1	VAA1_PSINU	Q04237	psilotum nu
396	2	7.1	30	1	VAA2_EQUAR	Q04238	equisetum a
397	2	7.1	30	1	VAA2_PSINU	Q04239	psilotum nu
398	2	7.1	30	1	VATN_BOVIN	P81134	bos taurus
399	2	7.1	30	1	VG03_BPPF1	P25137	bacterioph
400	2	7.1	30	1	VPU_HV1SC	P05948	human immun
401	2	7.1	30	1	VTTA_BPT3	P20837	bacterioph
402	2	7.1	30	1	Y161_TREPA	O83196	treponema p
403	2	7.1	30	1	Y357_BORBU	O51332	borrelia bu
404	2	7.1	30	1	Y425_BORBU	O51386	borrelia bu
405	2	7.1	30	1	Y523_BORBU	O51473	borrelia bu
406	2	7.1	30	1	Y573_TREPA	O83583	treponema p
407	2	7.1	30	1	Y932_TREPA	O83902	treponema p
408	2	7.1	30	1	YCCB_ECOLI	P24244	escherichia
409	2	7.1	31	1	A98A_DROME	O46201	drosophila
410	2	7.1	31	1	ANP3_PAGBO	P02732	pagotheria
411	2	7.1	31	1	BCAM_PIG	O19098	sus scrofa
412	2	7.1	31	1	CEC1_PIG	P14661	sus scrofa
413	2	7.1	31	1	CIRB_CHAPA	P56879	chassalia p
414	2	7.1	31	1	COG5_BOVIN	P83437	bos taurus
415	2	7.1	31	1	CTRP_PENMO	P35002	penaeus mon
416	2	7.1	31	1	CTX2_CORVA	P82601	coremiocnem

417	2	7.1	31	1	CU54_LOCMI	P11738	locusta mig
418	2	7.1	31	1	CXMA_CONMR	P56708	conus marmo
419	2	7.1	31	1	CYLA_PSYLO	P56872	psychotria
420	2	7.1	31	1	CY06_VIOOD	P58438	viola odora
421	2	7.1	31	1	CY0B_VIOOD	P58443	viola odora
422	2	7.1	31	1	DEF2_MESAU	P81466	mesocricetu
423	2	7.1	31	1	DIUX_DIPPU	P82372	diploptera
424	2	7.1	31	1	ENDB_CAMDR	P01203	camelus dro
425	2	7.1	31	1	ER29_BOVIN	P81623	bos taurus
426	2	7.1	31	1	GT_SERMA	P22416	serratia ma
427	2	7.1	31	1	GUN2_SCLSC	P21834	sclerotinia
428	2	7.1	31	1	H13_WHEAT	P15872	triticum ae
429	2	7.1	31	1	HBA_MACEU	P81043	macropus eu
430	2	7.1	31	1	HCY1_HOMAM	P82296	homarus ame
431	2	7.1	31	1	HCY2_MAISQ	P82303	maia squina
432	2	7.1	31	1	HEM2_PHAGO	P27687	phascolopsi
433	2	7.1	31	1	LC70_LACPA	P80959	lactobacill
434	2	7.1	31	1	LCCB_LEUME	P81052	leuconostoc
435	2	7.1	31	1	LPL_BUCRP	Q53017	buchnera ap
436	2	7.1	31	1	LPRM_ECOLI	P10739	escherichia
437	2	7.1	31	1	MALK_PHOLU	P41124	photorhabdu
438	2	7.1	31	1	MDH_STRAR	P19982	streptomyce
439	2	7.1	31	1	PETL_ANASP	Q8yvq2	anabaena sp
440	2	7.1	31	1	PETL_ARATH	P56776	arabidopsis
441	2	7.1	31	1	PETL_BETVU	P46612	beta vulgar
442	2	7.1	31	1	PETL_CHLVU	P56306	chlorella v
443	2	7.1	31	1	PETL_GUITH	O78468	guillardia
444	2	7.1	31	1	PETL_LOTJA	Q9bbr4	lotus japon
445	2	7.1	31	1	PETL_MAIZE	P19445	zea mays (m
446	2	7.1	31	1	PETL_MARPO	P12179	marchantia
447	2	7.1	31	1	PETL_MESVI	Q9mun4	mesostigma
448	2	7.1	31	1	PETL_NEPOL	Q9tky9	nephroselmi
449	2	7.1	31	1	PETL_OENHO	Q9mtk4	oenothera h
450	2	7.1	31	1	PETL_ORYSA	P12180	oryza sativ
451	2	7.1	31	1	PETL_POPDE	O20272	populus del
452	2	7.1	31	1	PETL_PORPU	P51221	porphyra pu
453	2	7.1	31	1	PETL_PSINU	Q8wi03	psilotum nu
454	2	7.1	31	1	PETL_SPIOL	Q9m310	spinacia ol
455	2	7.1	31	1	PETL_TOBAC	P12181	nicotiana t
456	2	7.1	31	1	PETL_WHEAT	P58247	triticum ae
457	2	7.1	31	1	PETM_CYACA	Q9t1r5	cyanidium c
458	2	7.1	31	1	PETN_CYACA	Q9t1r6	cyanidium c
459	2	7.1	31	1	PSAK_ANAVA	P23317	anabaena va
460	2	7.1	31	1	PSAM_CHLVU	P56314	chlorella v
461	2	7.1	31	1	PSAM_CYAPA	P48185	cyanophora
462	2	7.1	31	1	PSAM_SYNEL	P25903	synechococc
463	2	7.1	31	1	PSAM_SYNY3	P72986	synechocyst
464	2	7.1	31	1	PSBK_SYNVU	P19054	synechococc
465	2	7.1	31	1	PSBM_MESVI	Q9muq7	mesostigma
466	2	7.1	31	1	PSBT_CHLRE	P37256	chlamydomon
467	2	7.1	31	1	PSBT_CHLVU	P56327	chlorella v
468	2	7.1	31	1	PSBT_CYAPA	P48109	cyanophora
469	2	7.1	31	1	PSBT_EUGGR	P20176	euglena gra
470	2	7.1	31	1	PSBT_MESVI	Q9muv6	mesostigma
471	2	7.1	31	1	PSBT_PORPU	P51323	porphyra pu
472	2	7.1	31	1	PYSG_METBA	P80523	methanosarc
473	2	7.1	31	1	RECX_METCL	P37865	methylomona

474	2	7.1	31	1	RL21_STRTR	P48956 streptococc
475	2	7.1	31	1	SARL_HUMAN	O00631 homo sapien
476	2	7.1	31	1	SARL_MOUSE	Q9cqd6 mus musculu
477	2	7.1	31	1	SARL_RABIT	P42532 oryctolagus
478	2	7.1	31	1	SC37_MESMA	P83407 mesobuthus
479	2	7.1	31	1	SODC_STRHE	P81163 striga herm
480	2	7.1	31	1	Y191_BORBU	O51209 borrelia bu
481	2	7.1	31	1	Y603_ARCFU	O29652 archaeoglob
482	2	7.1	31	1	Y822_BORBU	O51762 borrelia bu
483	2	7.1	32	1	ADHR_DROYA	P28487 drosophila
484	2	7.1	32	1	APL3_DIAGR	P81471 diatraea gr
485	2	7.1	32	1	ATP0_PIG	P80021 sus scrofa
486	2	7.1	32	1	ATP7_SPIOL	P80088 spinacia ol
487	2	7.1	32	1	ATPO_SPIOL	P80087 spinacia ol
488	2	7.1	32	1	B4G1_RAT	P80225 r beta-1,4-
489	2	7.1	32	1	CAAP_MICEC	P21162 micromonosp
490	2	7.1	32	1	CAL0_BOVIN	P01260 bos taurus
491	2	7.1	32	1	CAL0_PIG	P01259 sus scrofa
492	2	7.1	32	1	CAPP_METEX	Q49136 methylobact
493	2	7.1	32	1	CEC_OIKKI	P83420 oiketicus k
494	2	7.1	32	1	COA1_BPIF1	O80295 bacterioph
495	2	7.1	32	1	COA1_BPIKE	P03676 bacterioph
496	2	7.1	32	1	COA2_BPFD	P03677 bacterioph
497	2	7.1	32	1	COA2_BPIF1	O80296 bacterioph
498	2	7.1	32	1	CRP_PLEPL	P12245 pleuronecte
499	2	7.1	32	1	CY31_DESAC	P81078 desulfuromo
500	2	7.1	32	1	CYBL_RHOGR	P32953 rhodotorula
501	2	7.1	32	1	CYSB_FASHE	P80529 fasciola he
502	2	7.1	32	1	ER29_CHICK	P81628 gallus gall
503	2	7.1	32	1	ER29_TRIVU	P81629 trichosurus
504	2	7.1	32	1	FER_PORCR	P18821 porphyridiu
505	2	7.1	32	1	FF21_SALEN	P55224 salmonella
506	2	7.1	32	1	FRIH_ANAPL	P80145 anas platyr
507	2	7.1	32	1	GHR4_RAT	P33581 rattus norv
508	2	7.1	32	1	GLB4_LAMSP	P20413 lamellibrac
509	2	7.1	32	1	GT82_DICLA	P82608 dicentrarch
510	2	7.1	32	1	H2AZ_ONCMY	P22647 oncorhynch
511	2	7.1	32	1	HCYC_CHEDE	P83172 cherax dest
512	2	7.1	32	1	IAPP_BOVIN	Q28207 bos taurus
513	2	7.1	32	1	IAPP_SAGOE	Q28934 saguinus oe
514	2	7.1	32	1	IAPP_SHEEP	Q28605 ovis aries
515	2	7.1	32	1	ITR2_CUCSA	P10291 cucumis sat
516	2	7.1	32	1	ITR3_CUCPE	P10293 cucurbita p
517	2	7.1	32	1	ITR4_CUCMA	P07853 cucurbita m
518	2	7.1	32	1	LEC_DOLAX	P02875 dolichos ax
519	2	7.1	32	1	LPID_ECOLI	P03060 escherichia
520	2	7.1	32	1	LPID_EDWTA	P08140 edwardsiell
521	2	7.1	32	1	LPIV_ECOLI	P03061 escherichia
522	2	7.1	32	1	MDH_NITAL	P10887 nitzschia a
523	2	7.1	32	1	NEUB_PIG	P01297 sus scrofa
524	2	7.1	32	1	OVOS_ANAPL	P20739 anas platyr
525	2	7.1	32	1	PA22_AGKHP	P18997 agkistrodon
526	2	7.1	32	1	PA2_RHONO	P43318 rhopilema n
527	2	7.1	32	1	PETL_CHLRE	P50369 chlamydomon
528	2	7.1	32	1	PETM_GUI TH	O78499 guillardia
529	2	7.1	32	1	PETM_PORPU	P51275 porphyra pu
530	2	7.1	32	1	PHNS_DESMU	P13062 desulfovibr

531	2	7.1	32	1	PHSS_DESBN	P13064	desulfovibr
532	2	7.1	32	1	PRT4_SCYCA	P30259	scyliorhinu
533	2	7.1	32	1	PRTE_HALME	P28308	halobacteri
534	2	7.1	32	1	PSBQ_PEA	P19589	pisum sativ
535	2	7.1	32	1	PSBT_CYACA	O19927	cyanidium c
536	2	7.1	32	1	PSBT_GUITH	O78512	guillardia
537	2	7.1	32	1	PSBT_ODOSI	P49516	odontella s
538	2	7.1	32	1	PSBZ_EUGAN	Q8s195	euglena ana
539	2	7.1	32	1	PSBZ_EUGGA	Q8s193	euglena gra
540	2	7.1	32	1	PSBZ_EUGMY	Q8s191	euglena myx
541	2	7.1	32	1	PSBZ_EUGST	Q8s189	euglena ste
542	2	7.1	32	1	PSBZ_EUGVI	Q8s187	euglena vir
543	2	7.1	32	1	RIP2_PHYDI	P34967	phytolacca
544	2	7.1	32	1	RS19_YEREN	Q56847	yersinia en
545	2	7.1	32	1	SCK2_CENNO	P58504	centruroides
546	2	7.1	32	1	TAT_SIVM2	P05912	simian immu
547	2	7.1	32	1	TRYP_PENMO	P35050	penaeus mon
548	2	7.1	32	1	TX29_PHONI	P29426	phoneutria
549	2	7.1	32	1	TXP7_APTSC	P49271	aptostichus
550	2	7.1	32	1	Y169_TREPA	O83199	treponema p
551	2	7.1	32	1	Y433_BORBU	O51394	borrelia bu
552	2	7.1	32	1	YCPG_MASLA	P29735	mastigoclad
553	2	7.1	32	1	YL55_CAEEL	P34435	caenorhabdi
554	2	7.1	32	1	YSCA_YEREN	Q01242	yersinia en
555	2	7.1	32	1	YTK3_ILTVT	P23985	infectious
556	2	7.1	33	1	ACT_DICVI	Q24733	dictyocaulu
557	2	7.1	33	1	ALOX_PICPA	P04842	pichia past
558	2	7.1	33	1	ANP3_MYOSC	P04367	myoxocephal
559	2	7.1	33	1	ANP5_MYOAE	P20421	myoxocephal
560	2	7.1	33	1	ATP7_SOLTU	P80496	solanum tub
561	2	7.1	33	1	BR2A_RANES	P40837	rana escule
562	2	7.1	33	1	BR2B_RANES	P40838	rana escule
563	2	7.1	33	1	BR2E_RANES	P32413	rana escule
564	2	7.1	33	1	BR2_RANBP	P32424	rana brevip
565	2	7.1	33	1	CECB_HELVI	P83414	heliopsis v
566	2	7.1	33	1	CECC_HELVI	P83415	heliopsis v
567	2	7.1	33	1	COA1_BPFD	P03675	bacterioph
568	2	7.1	33	1	COXL_ONCMY	P80330	oncorhynch
569	2	7.1	33	1	CU89_HUMAN	P59042	homo sapien
570	2	7.1	33	1	CXO_CONVE	P83301	conus ventr
571	2	7.1	33	1	DBB2_DOLAU	P83376	dolabella a
572	2	7.1	33	1	DEF4_MESAU	P81468	mesocricetu
573	2	7.1	33	1	DHE3_PIG	P42174	sus scrofa
574	2	7.1	33	1	FABI_RHASA	P81175	rhamdia sap
575	2	7.1	33	1	FER_PORAE	P18820	porphyridiu
576	2	7.1	33	1	GAST_CAVPO	P06885	cavia porce
577	2	7.1	33	1	GAST_CHIBR	P10034	chinchilla
578	2	7.1	33	1	GGN2_RANRU	P80396	rana rugosa
579	2	7.1	33	1	GGN3_RANRU	P80397	rana rugosa
580	2	7.1	33	1	GLU2_ORENI	P81027	oreochromis
581	2	7.1	33	1	HF40_MAIZE	P82865	zea mays (m
582	2	7.1	33	1	HOXU_RHOOP	P22659	rhodococcus
583	2	7.1	33	1	LPPY_SALTY	P08522	salmonella
584	2	7.1	33	1	LPRH_ECOLI	P37324	escherichia
585	2	7.1	33	1	LYC2_HORSE	P81710	equus cabal
586	2	7.1	33	1	MHAA_STRCH	P80435	streptomyce
587	2	7.1	33	1	MYMY_MYTED	P81614	mytilus edu

588	2	7.1	33	1	OTCC_PSEPU
589	2	7.1	33	1	PAP1_PARPV
590	2	7.1	33	1	PAP2_PARPV
591	2	7.1	33	1	PAP3_PARPV
592	2	7.1	33	1	PAP4_PARMA
593	2	7.1	33	1	PAP5_PARMA
594	2	7.1	33	1	PEN3_ADECU
595	2	7.1	33	1	PETM_CYAPA
596	2	7.1	33	1	PETM_SYNEL
597	2	7.1	33	1	PK1_DICDI
598	2	7.1	33	1	PK5_DICDI
599	2	7.1	33	1	PRTL_ECOLI
600	2	7.1	33	1	PSAI_SPIOL
601	2	7.1	33	1	PSAK_CUCSA
602	2	7.1	33	1	PSBT_ARATH
603	2	7.1	33	1	PSBT_MAIZE
604	2	7.1	33	1	RL21_XENLA
605	2	7.1	33	1	RL26_XENLA
606	2	7.1	33	1	RL28_XENLA
607	2	7.1	33	1	RL4_HALCU
608	2	7.1	33	1	RPOC_HETCA
609	2	7.1	33	1	RRPO_BPBZ1
610	2	7.1	33	1	RS4_XENLA
611	2	7.1	33	1	RT25_BOVIN
612	2	7.1	33	1	RUGA_RANRU
613	2	7.1	33	1	SC63_CANFA
614	2	7.1	33	1	T1F_PARTE
615	2	7.1	33	1	TXH1_SELHU
616	2	7.1	33	1	TXN3_SELHA
617	2	7.1	33	1	VT1B_RAT
618	2	7.1	33	1	Y656_TREPA
619	2	7.1	33	1	Y849_BORBU
620	2	7.1	33	1	YC12_CHLRE
621	2	7.1	33	1	YC12_EUGGR
622	2	7.1	33	1	YC12_MARPO
623	2	7.1	33	1	YC12_MESVI
624	2	7.1	33	1	YC12_NEPOL
625	2	7.1	33	1	YC12_PINTH
626	2	7.1	33	1	YL74_ARCFU
627	2	7.1	33	1	YLCH_ECOLI
628	2	7.1	34	1	AMP2_CHICK
629	2	7.1	34	1	ASPG_PIG
630	2	7.1	34	1	BR2C_RANES
631	2	7.1	34	1	COL_CHICK
632	2	7.1	34	1	COXA_THETH
633	2	7.1	34	1	COXG_THUOB
634	2	7.1	34	1	CXGS_CONGE
635	2	7.1	34	1	DEF2_RABIT
636	2	7.1	34	1	DMS1_PHYSA
637	2	7.1	34	1	DMS2_PHYSA
638	2	7.1	34	1	ECAB_ECTTU
639	2	7.1	34	1	EGGR_APLCA
640	2	7.1	34	1	EM1_ENSMI
641	2	7.1	34	1	GAST_CAPHI
642	2	7.1	34	1	GUN1_SCLSC
643	2	7.1	34	1	H1S_STRPU
644	2	7.1	34	1	HEMO_CHICK

P11727	pseudomonas
P81865	pardachirus
P23067	pardachirus
P81866	pardachirus
P81861	pardachirus
P81862	pardachirus
P35987	canine aden
P48366	cyanophora
Q8dj15	synechococc
P34101	dictyosteli
P34104	dictyosteli
P02338	escherichia
P17228	spinacia ol
P42051	cucumis sat
P37259	arabidopsis
P37257	zea mays (m
P49628	xenopus lae
P49629	xenopus lae
P46780	xenopus lae
P05967	halobacteri
P36441	heterosigma
P09674	bacterioph
P49401	xenopus lae
P82669	bos taurus
P80954	rana rugosa
P82008	canis famil
Q27172	paramecium
P56676	selenocosmi
P83464	selenocosmi
P58200	rattus norv
O83662	treponema p
O51789	borrelia bu
P50370	chlamydomon
P31559	euglena gra
P31560	marchantia
Q9mus3	mesostigma
Q9tky6	nephroselmi
P41600	pinus thunb
O28108	archaeoglob
Q47268	escherichia
P80390	gallus gall
P30918	sus scrofa
P40839	rana escule
P11148	gallus gall
P82543	thermus the
P80976	thunnus obe
P15472	conus geogr
P07468	oryctolagus
P24302	phyllomedus
P80278	phyllomedus
P49344	ectatomma t
P01363	aplysia cal
P27205	ensis minor
P04564	capra hircu
P21833	sclerotinia
P19376	strongyloce
P20057	gallus gall

645	2	7.1	34	1	HS7S_CUCMA	P31082	cucurbita m
646	2	7.1	34	1	ITR1_MOMCO	P82408	momordica c
647	2	7.1	34	1	ITR2_MOMCO	P82409	momordica c
648	2	7.1	34	1	LPTN_PROVU	P28779	proteus vul
649	2	7.1	34	1	M44E_HUMAN	Q96pg1	homo sapien
650	2	7.1	34	1	MYTA_MYTED	P81612	mytilus edu
651	2	7.1	34	1	MYTB_MYTED	P81613	mytilus edu
652	2	7.1	34	1	PETM_ANASP	Q9f4w2	anabaena sp
653	2	7.1	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
654	2	7.1	34	1	PSAI_OENHO	Q9mtl2	oenothera h
655	2	7.1	34	1	PSBM_ARATH	P12169	arabidopsis
656	2	7.1	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
657	2	7.1	34	1	PSBM_CHLRE	P92277	chlamydomon
658	2	7.1	34	1	PSBM_MAIZE	P48189	zea mays (m
659	2	7.1	34	1	PSBM_MARPO	P12168	marchantia
660	2	7.1	34	1	PSBM_OENHO	Q9mtm8	oenothera h
661	2	7.1	34	1	PSBM_PEA	P34833	pisum sativ
662	2	7.1	34	1	PSBM_PSINU	Q8wi22	psilotum nu
663	2	7.1	34	1	PSBM_WHEAT	Q9xps6	triticum ae
664	2	7.1	34	1	PSBT_TOBAC	P12184	nicotiana t
665	2	7.1	34	1	PSPC_BOVIN	P15783	bos taurus
666	2	7.1	34	1	PSPC_CANFA	P22397	canis famil
667	2	7.1	34	1	PTU1_PEITU	P58606	peirates tu
668	2	7.1	34	1	PYSB_METBA	P80522	methanosarc
669	2	7.1	34	1	RNL1_PIG	P15466	sus scrofa
670	2	7.1	34	1	SCXM_SCOMA	P80719	scorpio mau
671	2	7.1	34	1	SMS_MYXGL	P19209	myxine glut
672	2	7.1	34	1	THEM_MALSU	P13858	malbranchea
673	2	7.1	34	1	TX1_SCOGR	P56855	scodra gris
674	2	7.1	34	1	TX33_PHONI	P81789	phoneutria
675	2	7.1	34	1	TXP5_BRASM	P49266	brachypelma
676	2	7.1	34	1	VLYS_BPM1	P08229	bacterioph
677	2	7.1	34	1	VPU_HV1W2	P08808	human immun
678	2	7.1	34	1	Y05J_BPT4	P39239	bacterioph
679	2	7.1	34	1	Y224_TREPA	O83253	treponema p
680	2	7.1	34	1	Y848_BORBU	O51788	borrelia bu
681	2	7.1	34	1	Y870_HAEIN	P44065	haemophilus
682	2	7.1	34	1	Y967_HAEIN	P44086	haemophilus
683	2	7.1	34	1	YC12_PORPU	P51385	porphyra pu
684	2	7.1	34	1	YC12_SKECO	O96797	skeletonema
685	2	7.1	34	1	YMIA_AGRTU	P38437	agrobacteri
686	2	7.1	34	1	Z33B_HUMAN	Q06731	homo sapien
687	2	7.1	35	1	ADO1_AGRDO	P58608	agriosphodr
688	2	7.1	35	1	C550_BACHA	P80091	bacillus ha
689	2	7.1	35	1	CECA_HELVI	P83413	heliolithis v
690	2	7.1	35	1	CECB_ANTPE	P01509	antheraea p
691	2	7.1	35	1	CHI1_CASSA	P29137	castanea sa
692	2	7.1	35	1	CPI2_PIG	P80736	sus scrofa
693	2	7.1	35	1	D3HI_RABIT	P32185	oryctolagus
694	2	7.1	35	1	ERFK_KLEAE	Q08599	klebsiella
695	2	7.1	35	1	EXE2_HELSU	P04204	heloderma s
696	2	7.1	35	1	FAS_CAPHI	P08757	capra hircu
697	2	7.1	35	1	GBGU_MOUSE	Q61017	mus musculu
698	2	7.1	35	1	GP58_BPSP1	O48412	bacterioph
699	2	7.1	35	1	GRDB_CLOPU	P55793	clostridium
700	2	7.1	35	1	HCYA_CHEDE	P83173	cherax dest
701	2	7.1	35	1	HMWC_DESGI	P38588	desulfovibr

702	2	7.1	35	1	IAAC_HORVU	P34951	hordeum vul
703	2	7.1	35	1	KPPR_PINPS	P81664	pinus pinas
704	2	7.1	35	1	LCGB_LACLA	P36962	lactococcus
705	2	7.1	35	1	NEF_HV1H3	P05854	human immun
706	2	7.1	35	1	PBP1_LYMDI	P34176	lymantria d
707	2	7.1	35	1	PBP2_LYMDI	P34177	lymantria d
708	2	7.1	35	1	PBP_HYACE	P34175	hyalophora
709	2	7.1	35	1	PBP_ORGPS	P34178	orgyia pseu
710	2	7.1	35	1	PETG_CYACA	Q9tlq9	cyanidium c
711	2	7.1	35	1	PHI1_MYTCA	P35422	mytilus cal
712	2	7.1	35	1	PSAI_CYAPA	P48116	cyanophora
713	2	7.1	35	1	PSBT_MARPO	P12182	marchantia
714	2	7.1	35	1	PSBT_OENHO	P37258	oenothera h
715	2	7.1	35	1	PSBT_ORYSA	P12183	oryza sativ
716	2	7.1	35	1	PSBT_PINTH	P41625	pinus thunb
717	2	7.1	35	1	PSPC_PIG	P15785	sus scrofa
718	2	7.1	35	1	RL15_SYNP7	P31160	synechococc
719	2	7.1	35	1	RL32_HALCU	P05965	halobacteri
720	2	7.1	35	1	SCKK_TITSE	P56219	tityus serr
721	2	7.1	35	1	SCX1_BUTSI	P15229	buthus sind
722	2	7.1	35	1	SCX5_BUTEU	P15222	buthus eupe
723	2	7.1	35	1	SCXP_ANDMA	P01498	androctonus
724	2	7.1	35	1	SMS_LAMFL	Q9prro	lampetra fl
725	2	7.1	35	1	SPRC_PIG	P20112	sus scrofa
726	2	7.1	35	1	THPA_THADA	P21381	thaumatococ
727	2	7.1	35	1	TMTX_MESTA	Q9bn12	mesobuthus
728	2	7.1	35	1	TX1_GRASP	P56852	grammostola
729	2	7.1	35	1	TX1_THRPR	P83480	thrixopelma
730	2	7.1	35	1	TX2_GRASP	P56853	grammostola
731	2	7.1	35	1	TXAG_AGEOP	P31328	agelena opu
732	2	7.1	35	1	TXH4_SELHU	P83303	selenocosmi
733	2	7.1	35	1	TXKS_STOHE	P29187	stoichactis
734	2	7.1	35	1	TXN4_SELHA	P83471	selenocosmi
735	2	7.1	35	1	VL3_PAPVD	P06919	deer papill
736	2	7.1	35	1	VORB_METTM	P80908	methanobact
737	2	7.1	35	1	VSPA_CERVI	P18692	cerastes vi
738	2	7.1	35	1	WSP7_PINPS	P81086	pinus pinas
739	2	7.1	35	1	Y210_HAEIN	P43964	haemophilus
740	2	7.1	35	1	Y320_BORBU	O51299	borrelia bu
741	2	7.1	35	1	Y37_BPT3	P20325	bacteriopha
742	2	7.1	35	1	Y845_BORBU	O51785	borrelia bu
743	2	7.1	35	1	Y847_BORBU	O51787	borrelia bu
744	2	7.1	35	1	YC12_CYACA	Q9tlx0	cyanidium c
745	2	7.1	35	1	YC69_ARCFU	O28999	archaeoglob
746	2	7.1	35	1	YRKM_BACSU	P54440	bacillus su
747	2	7.1	36	1	AMPL_PIG	P28839	sus scrofa
748	2	7.1	36	1	ANFV_ANGJA	P22642	anguilla ja
749	2	7.1	36	1	C3L1_BOVIN	P30922	bos taurus
750	2	7.1	36	1	CBBA_NITVU	P37102	nitrobacter
751	2	7.1	36	1	CECD_ANTPE	P01511	antheraea p
752	2	7.1	36	1	CYC7_GEOME	P81894	geobacter m
753	2	7.1	36	1	F4RE_METOG	P80951	methanogeni
754	2	7.1	36	1	GLU1_ORENI	P81026	oreochromis
755	2	7.1	36	1	GLUC_HYDCO	P09682	hydrolagus
756	2	7.1	36	1	H1L5_ENSMI	P27203	ensis minor
757	2	7.1	36	1	HBB_PONPY	Q9tt34	pongo pygma
758	2	7.1	36	1	IOB1_ISYOB	P58609	isyndus obs

759	2	7.1	36	1	KAD_STRGR	P53398	streptomyce
760	2	7.1	36	1	LHG_RHOVI	P04126	rhodopseudo
761	2	7.1	36	1	LYOX_PIG	P45845	sus scrofa
762	2	7.1	36	1	MFA1_YEAST	P34165	saccharomyc
763	2	7.1	36	1	MPG2_DACGL	Q41183	dactylis gl
764	2	7.1	36	1	MYPC_RAT	P56741	rattus norv
765	2	7.1	36	1	NEUH_CARCA	P11975	cardisoma c
766	2	7.1	36	1	NEUY_GADMO	P80167	gadus morhu
767	2	7.1	36	1	NEUY_ONCMY	P29071	oncorhynchu
768	2	7.1	36	1	NEUY_RABIT	P09640	oryctolagus
769	2	7.1	36	1	NEUY_RANRI	P29949	rana ridibu
770	2	7.1	36	1	NLTP_PINPI	P26912	pinus pinea
771	2	7.1	36	1	NPF_ARTTR	P41334	artioposthi
772	2	7.1	36	1	NUCM_SOLTU	P80264	solanum tub
773	2	7.1	36	1	OST2_CHICK	P80897	gallus gall
774	2	7.1	36	1	OSTS_YEAST	Q99380	saccharomyc
775	2	7.1	36	1	PAHO_ALLMI	P06305	alligator m
776	2	7.1	36	1	PAHO_CHIBR	P41519	chinchilla
777	2	7.1	36	1	PAHO_LARAR	P41337	larus argen
778	2	7.1	36	1	PAHO_RANCA	P15427	rana catesb
779	2	7.1	36	1	PAHO_RANTE	P31229	rana tempor
780	2	7.1	36	1	PAHO_STRCA	P11967	struthio ca
781	2	7.1	36	1	PETM_SYNY3	P74810	synechocyst
782	2	7.1	36	1	PGKH_CHLFU	P36232	chlorella f
783	2	7.1	36	1	PMY_PETMA	P80024	petromyzon
784	2	7.1	36	1	PSAH_PEA	P20121	pisum sativ
785	2	7.1	36	1	PSAI_ANGLY	P28251	angiopteris
786	2	7.1	36	1	PSAI_CARCL	Q9gdv2	carpobrotus
787	2	7.1	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
788	2	7.1	36	1	PSAI_CHLVU	P58214	chlorella v
789	2	7.1	36	1	PSAI_CYACA	Q9tm24	cyanidium c
790	2	7.1	36	1	PSAI_GUITH	O78462	guillardia
791	2	7.1	36	1	PSAI_HORVU	P13165	hordeum vul
792	2	7.1	36	1	PSAI_MAIZE	P30980	zea mays (m
793	2	7.1	36	1	PSAI_MARPO	P12185	marchantia
794	2	7.1	36	1	PSAI_MESVI	Q9muq4	mesostigma
795	2	7.1	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
796	2	7.1	36	1	PSAI_ORYSA	P12186	oryza sativ
797	2	7.1	36	1	PSAI_PICAB	O47040	picea abies
798	2	7.1	36	1	PSAI_PORPU	P51387	porphyra pu
799	2	7.1	36	1	PSAI_PSINU	Q8wi10	psilotum nu
800	2	7.1	36	1	PSAI_WHEAT	P25410	triticum ae
801	2	7.1	36	1	PSBI_ARATH	P09970	arabidopsis
802	2	7.1	36	1	PSBI_HORVU	P25876	hordeum vul
803	2	7.1	36	1	PSBI_MARPO	P09969	marchantia
804	2	7.1	36	1	PSBI_ORYSA	P12161	oryza sativ
805	2	7.1	36	1	PSBI_PINTH	P41599	pinus thunb
806	2	7.1	36	1	PSBI_PSEMZ	P29796	pseudotsuga
807	2	7.1	36	1	PSBM_CHLVU	P56325	chlorella v
808	2	7.1	36	1	PSBY_ODOSI	P49543	odontella s
809	2	7.1	36	1	PSBY_PORPU	P51206	porphyra pu
810	2	7.1	36	1	PYY_AMICA	P29205	amia calva
811	2	7.1	36	1	PYY_LEPSP	P09473	lepisosteus
812	2	7.1	36	1	PYY_MYOSC	P09641	myoxocephal
813	2	7.1	36	1	PYY_ONCKI	P09474	oncorhynchu
814	2	7.1	36	1	PYY_ORENI	P81028	oreochromis
815	2	7.1	36	1	PYY_PIG	P01305	sus scrofa

816	2	7.1	36	1	PYY_RAJRH
817	2	7.1	36	1	PYY_RANRI
818	2	7.1	36	1	R18A_BOVIN
819	2	7.1	36	1	RET4_CHICK
820	2	7.1	36	1	RL6_HALCU
821	2	7.1	36	1	SCK2_CENLL
822	2	7.1	36	1	SCK3_LEIQH
823	2	7.1	36	1	SCX1_BUTEU
824	2	7.1	36	1	SCX8_BUTOE
825	2	7.1	36	1	SCXL_LEIQU
826	2	7.1	36	1	SPYY_PHYBI
827	2	7.1	36	1	TAEK_ACTEQ
828	2	7.1	36	1	TERN_PSEUS
829	2	7.1	36	1	TLN1_CHICK
830	2	7.1	36	1	TX1B_AGEAP
831	2	7.1	36	1	TXAM_METSE
832	2	7.1	36	1	TXD3_PARLU
833	2	7.1	36	1	Y16L_BPT4
834	2	7.1	36	1	Y260_BACHD
835	2	7.1	36	1	Y609_ARCFU
836	2	7.1	36	1	Y699_TREPA
837	2	7.1	36	1	YC12_CYAPA
838	2	7.1	36	1	YG50_HAEIN
839	2	7.1	36	1	YRKG_BACSU
840	2	7.1	37	1	24KD_PLACH
841	2	7.1	37	1	AFP4_MALPA
842	2	7.1	37	1	ANP3_PSEAM
843	2	7.1	37	1	ATPO_SOLTU
844	2	7.1	37	1	B2MG_ORENI
845	2	7.1	37	1	CAL1_PIG
846	2	7.1	37	1	CAL1_SHEEP
847	2	7.1	37	1	CALR_RANRI
848	2	7.1	37	1	CEC2_MANSE
849	2	7.1	37	1	CEC3_MANSE
850	2	7.1	37	1	CEC4_MANSE
851	2	7.1	37	1	CG2S_LUPAN
852	2	7.1	37	1	CHCD_ANTPO
853	2	7.1	37	1	CUP4_SARBU
854	2	7.1	37	1	DIU1_TENMO
855	2	7.1	37	1	ECAA_ECTTU
856	2	7.1	37	1	F13A_BOVIN
857	2	7.1	37	1	GHR3_RAT
858	2	7.1	37	1	HCYB_CANPG
859	2	7.1	37	1	HOXF_RHOOP
860	2	7.1	37	1	LCNM_LACLA
861	2	7.1	37	1	LPPY_SERMA
862	2	7.1	37	1	MAUR_PARVE
863	2	7.1	37	1	ME20_EUPRA
864	2	7.1	37	1	ME22_EUPRA
865	2	7.1	37	1	MIBP_PSESP
866	2	7.1	37	1	NLT3_VITSX
867	2	7.1	37	1	NUFM_SOLTU
868	2	7.1	37	1	OP2A_OXYKI
869	2	7.1	37	1	OP2C_OXYKI
870	2	7.1	37	1	OP2D_OXYKI
871	2	7.1	37	1	PETG_ANASP
872	2	7.1	37	1	PETG_ANAVA

P29206	raja	rhina
P29204	rana	ridibu
P82919	bos	taurus
P30370	gallus	gall
P05968	halobacteri	
P45630	centruroide	
P45660	leiurus	qui
P15220	buthus	eupe
P04098	buthus	occi
P45639	leiurus	qui
P80952	phyllomedus	
P81897	actinia	equ
P82321	pseudacanth	
P54939	gallus	gall
P15970	agelenopsis	
P11495	metridium	s
P83258	paracoelote	
P39244	bacterioph	
Q9kg53	bacillus	ha
O29646	archaeoglob	
O83697	treponema	p
P48256	cyanophora	
P44281	haemophilus	
P54434	bacillus	su
P14592	plasmodium	
P83138	malva	parvi
P02733	pseudopleur	
P80504	solanum	tub
Q03423	oreochromis	
P30880	sus	scrofa
P30881	ovis	aries
P31888	rana	ridibu
P14662	manduca	sex
P14663	manduca	sex
P14664	manduca	sex
P09930	lupinus	ang
P08931	antheraea	p
P14486	sarcophaga	
P56618	tenebrio	mo
P49343	ectatomma	t
P12260	bos	taurus
P33580	rattus	norv
P83175	cancer	pagu
P22658	rhodococcus	
P83002	lactococcus	
P19937	serratia	ma
Q56462	paracoccus	
P26888	euplotes	ra
P58548	euplotes	ra
P04576	pseudomonas	
P80273	vitis	sp. (
P80266	solanum	tub
P83248	oxyopes	kit
P83250	oxyopes	kit
P83251	oxyopes	kit
P58246	anabaena	sp
Q913p7	anabaena	va

873	2	7.1	37	1	PETG_ARATH	P56775	arabidopsis
874	2	7.1	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
875	2	7.1	37	1	PETG_CHLEU	P46304	chlamydomon
876	2	7.1	37	1	PETG_CHLRE	Q08362	chlamydomon
877	2	7.1	37	1	PETG_CHLVU	P56305	chlorella v
878	2	7.1	37	1	PETG_CUSRE	P30398	cuscuta ref
879	2	7.1	37	1	PETG_CYAPA	P14236	cyanophora
880	2	7.1	37	1	PETG_EUGGR	P30396	euglena gra
881	2	7.1	37	1	PETG_GUIITH	O78505	guillardia
882	2	7.1	37	1	PETG_MARPO	P12120	marchantia
883	2	7.1	37	1	PETG_MESVI	Q9mun3	mesostigma
884	2	7.1	37	1	PETG_NEPOL	Q9tky8	nephroselmi
885	2	7.1	37	1	PETG_ODOSI	P49470	odontella s
886	2	7.1	37	1	PETG_ORYSA	P12121	oryza sativ
887	2	7.1	37	1	PETG_PINTH	P41614	pinus thunb
888	2	7.1	37	1	PETG_PORPU	P51318	porphyra pu
889	2	7.1	37	1	PETG_PSINU	Q8wi02	psilotum nu
890	2	7.1	37	1	PETG_SKECO	O96811	skeletonema
891	2	7.1	37	1	PETG_SYNEL	Q8dki2	synechococc
892	2	7.1	37	1	PETG_SYNP7	Q9z3g1	synechococc
893	2	7.1	37	1	PIIL_ACHLY	P81720	achromobact
894	2	7.1	37	1	PIP7_BOVIN	P21671	bos taurus
895	2	7.1	37	1	PRF1_RAT	P18889	rattus norv
896	2	7.1	37	1	PSBL_ARATH	P29301	arabidopsis
897	2	7.1	37	1	PSBL_ORYSA	P12166	oryza sativ
898	2	7.1	37	1	PSBM_PINTH	P41608	pinus thunb
899	2	7.1	37	1	PSBY_CYACA	O19893	cyanidium c
900	2	7.1	37	1	PSBY_GUIITH	O78433	guillardia
901	2	7.1	37	1	PYY_CHICK	P29203	gallus gall
902	2	7.1	37	1	RK36_ASTLO	P24355	astasia lon
903	2	7.1	37	1	RK36_CHLVU	P56360	chlorella v
904	2	7.1	37	1	RK36_CYACA	Q9tlu9	cyanidium c
905	2	7.1	37	1	RK36_CYAPA	P48131	cyanophora
906	2	7.1	37	1	RK36_EUGGR	P21532	euglena gra
907	2	7.1	37	1	RK36_NEPOL	Q9tl26	nephroselmi
908	2	7.1	37	1	RK36_ODOSI	P49568	odontella s
909	2	7.1	37	1	RK36_PORPU	P51296	porphyra pu
910	2	7.1	37	1	RL36_AQUAE	O66487	aquifex aeo
911	2	7.1	37	1	RL36_BACHD	O50631	bacillus ha
912	2	7.1	37	1	RL36_BACSU	P20278	bacillus su
913	2	7.1	37	1	RL36_BORBU	O51452	borrelia bu
914	2	7.1	37	1	RL36_CAMJE	Q9pm84	campylobact
915	2	7.1	37	1	RL36_CLOAB	Q97ek2	clostridium
916	2	7.1	37	1	RL36_DEIRA	Q9rsk0	deinococcus
917	2	7.1	37	1	RL36_HELPJ	Q9zjt1	helicobacte
918	2	7.1	37	1	RL36_HELPY	P56058	helicobacte
919	2	7.1	37	1	RL36_LEPIN	Q9xd13	leptospira
920	2	7.1	37	1	RL36_LISMO	Q927n0	listeria mo
921	2	7.1	37	1	RL36_MYCGE	P47420	mycoplasma
922	2	7.1	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
923	2	7.1	37	1	RL36_MYCPU	Q98q05	mycoplasma
924	2	7.1	37	1	RL36_MYCSP	P38015	mycoplasma
925	2	7.1	37	1	RL36_MYCTU	P45810	mycobacteri
926	2	7.1	37	1	RL36_STAAM	Q99s42	staphylococ
927	2	7.1	37	1	RL36_STRCO	O86772	streptomyce
928	2	7.1	37	1	RL36_SYNP6	O24707	synechococc
929	2	7.1	37	1	RL36_THETH	P80256	thermus the

930	2	7.1	37	1	RL36_TREPA
931	2	7.1	37	1	RS15_HELLU
932	2	7.1	37	1	RUGC_RANRU
933	2	7.1	37	1	SCIT_MESTA
934	2	7.1	37	1	SCK3_BUTOC
935	2	7.1	37	1	SCK3_PARTR
936	2	7.1	37	1	SCKA_TITSE
937	2	7.1	37	1	SCKI_MESTA
938	2	7.1	37	1	SMS_PETMA
939	2	7.1	37	1	TCTP_TRYBB
940	2	7.1	37	1	THHS_HORVU
941	2	7.1	37	1	TX21_SELHU
942	2	7.1	37	1	TX3D_AGEAP
943	2	7.1	37	1	TXD1_PARLU
944	2	7.1	37	1	TXJC_HADVE
945	2	7.1	37	1	TXKB_BUNGR
946	2	7.1	37	1	TXOD_HADVE
947	2	7.1	37	1	TXP3_APTSC
948	2	7.1	37	1	VA1_BPBF2
949	2	7.1	37	1	VG40_BPML5
950	2	7.1	37	1	VGJ_BPPHX
951	2	7.1	37	1	VPU_HVIZ8
952	2	7.1	37	1	Y268_ARCFU
953	2	7.1	37	1	Y63_BPT3
954	2	7.1	37	1	Y63_BPT7
955	2	7.1	37	1	Y692_BORBU
956	2	7.1	37	1	Y700_BORBU
957	2	7.1	37	1	Y762_BORBU
958	2	7.1	37	1	Y846_BORBU
959	2	7.1	37	1	YBGT_ECOLI
960	2	7.1	37	1	YC12_CHLVU
961	2	7.1	37	1	YDA3_SCHPO
962	2	7.1	37	1	YIM4_BPPH1
963	2	7.1	37	1	YQGE_BACCA
964	2	7.1	37	1	YRYL_CAEEL
965	2	7.1	38	1	AFP5_MALPA
966	2	7.1	38	1	ATPO_PEA
967	2	7.1	38	1	BD01_BOVIN
968	2	7.1	38	1	BD08_BOVIN
969	2	7.1	38	1	BD11_BOVIN
970	2	7.1	38	1	COA3_XANCP
971	2	7.1	38	1	CPRP_CANPG
972	2	7.1	38	1	CU47_LACCU
973	2	7.1	38	1	DCHS_MICSP
974	2	7.1	38	1	DLP3_ORNAN
975	2	7.1	38	1	DPOB_BOVIN
976	2	7.1	38	1	E2F1_RAT
977	2	7.1	38	1	EST5_DROMO
978	2	7.1	38	1	EXE1_HELSU
979	2	7.1	38	1	FER_METPR
980	2	7.1	38	1	GLUM_HYDCO
981	2	7.1	38	1	GME1_RAT
982	2	7.1	38	1	H5_COLLI
983	2	7.1	38	1	HIS1_MACFA
984	2	7.1	38	1	HMG2_BOVIN
985	2	7.1	38	1	HOXH_RHOOP
986	2	7.1	38	1	ID5B_ADEPA

O83239	treponema p
P52820	helix lucor
P80956	rana rugosa
P81761	mesobuthus
P59290	buthus occi
P83112	parabuthus
P46114	tityus serr
P24663	mesobuthus
P21779	petromyzon
P35758	trypanosoma
P33045	hordeum vul
P82959	selenocosmi
P81746	agelenopsis
P83256	paracoelote
P82228	hadronyche
P29186	bunodosoma
P81597	hadronyche
P49268	aptostichus
P19347	bacterioph
Q05250	mycobacteri
P03651	bacterioph
P08807	human immun
O29971	archaeoglob
P20328	bacterioph
P03799	bacterioph
O51635	borrelia bu
O51643	borrelia bu
O51703	borrelia bu
O51786	borrelia bu
P56100	escherichia
P56328	chlorella v
Q10345	schizosacch
P10428	bacterioph
P28753	bacillus ca
Q19177	caenorhabdi
P83139	malva parvi
P17604	pisum sativ
P46159	bos taurus
P46166	bos taurus
P46169	bos taurus
Q07484	xanthomonas
P81033	cancer pagu
P80323	lactobacill
P00863	micrococcus
P82141	ornithorhyn
Q27958	bos taurus
O09139	rattus norv
P10095	drosophila
P04203	heloderma s
P81542	metallosp
P23063	hydrolagus
Q9quz8	rattus norv
P02260	columba liv
P34084	macaca fasc
P40673	bos taurus
P22661	rhodococcus
P09942	adenanthera

987	2	7.1	38	1	ID5B_PROJU	P32734	prosopsis j
988	2	7.1	38	1	MFA2_YEAST	P34166	saccharomyc
989	2	7.1	38	1	MUTS_YEREN	P47763	yersinia en
990	2	7.1	38	1	NLT1_VITSX	P80275	vitis sp. (
991	2	7.1	38	1	NLT2_VITSX	P33556	vitis sp. (
992	2	7.1	38	1	OBP2_HYSCR	P81648	hystrix cri
993	2	7.1	38	1	PA21_MATBI	P24644	maticora bi
994	2	7.1	38	1	PA22_MATBI	P24645	maticora bi
995	2	7.1	38	1	PACA_URAJA	P81039	uranoscopu
996	2	7.1	38	1	PETG_SYNY3	P74149	synechocyst
997	2	7.1	38	1	PHRG_BACSU	O32295	bacillus su
998	2	7.1	38	1	POI_MUSDO	P81765	musca domes
999	2	7.1	38	1	PSAI_ODOSI	P49484	odontella s
1000	2	7.1	38	1	PSAI_PROMA	O87786	prochloroco

ALIGNMENTS

RESULT 1

ELH_THETS

ID ELH_THETS STANDARD; PRT; 36 AA.

AC P80594;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Egg-laying-like hormone (L-ELH).

OS Theromyzon tessulatum (Leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Rhynchobdellida; Glossiphoniidae; Theromyzon.

OX NCBI_TaxID=13286;

RN [1]

RP SEQUENCE.

RC TISSUE=CNS;

RX MEDLINE=98047073; PubMed=9387880;

RA Salzert M., Verger-Bocquet M., Vandenbulcke F., van Minnen J.;

RT "Leech egg-laying-like hormone: structure, neuronal distribution and phylogeny.";

RL Brain Res. Mol. Brain Res. 49:211-221(1997).

CC -!- FUNCTION: MAY BE INVOLVED IN LEECH REPRODUCTION.

CC -!- TISSUE SPECIFICITY: SUPRA, SUBESOPHAGEAL GANGLIA AND SEGMENTAL GANGLIA OF THE VENTRAL NERVE CORD AND BRAIN.

CC -!- DEVELOPMENTAL STAGE: L-ELH GREATLY INCREASES BEFORE EGG-LAYING, WHILE IT STRONGLY DECREASES AFTER EGG-LAYING.

CC -!- MASS SPECTROMETRY: MW=4172.29; METHOD=Electrospray.

KW Hormone; Amidation; Neuropeptide.

FT MOD_RES 36 36 AMIDATION.

SQ SEQUENCE 36 AA; 4290 MW; 2633C40D6A15CECC CRC64;

Query Match 17.9%; Score 5; DB 1; Length 36;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRRF 16
 |||||
 Db 29 LRRRF 33

RESULT 2

PSAM_EUGGR

ID PSAM_EUGGR STANDARD; PRT; 31 AA.
AC P31479;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Photosystem I reaction centre subunit XII (PSI-M).
GN PSAM.
OS Euglena gracilis.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z / UTEX 753;
RX MEDLINE=93347989; PubMed=8346031;
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
RA Orsat B., Spielmann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA.";
RL Nucleic Acids Res. 21:3537-3544(1993).
CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
CC -----
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DR EMBL; X70810; CAA50083.1; -.
DR PIR; S34504; S34504.
KW Photosystem I; Photosynthesis; Chloroplast.
SQ SEQUENCE 31 AA; 3443 MW; 85F208627C873165 CRC64;

Query Match 14.3%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGKS 8
|||
Db 25 LGKS 28

RESULT 3

DEF7_RABIT

ID DEF7_RABIT STANDARD; PRT; 34 AA.
AC P80223; P80224;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Corticostatin VI (CS-VI) (Neutrophil antibiotic peptide NP-6).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Japanese white; TISSUE=Spleen;
 RX MEDLINE=93387318; PubMed=8397087;
 RA Fuse N., Hayashi Y., Fukata J., Tominaga T., Ebisui O., Satoh Y.,
 RA Isohara T., Uno I., Imura H.;
 RT "Purification and characterization of new anti-adrenocorticotropin
 RT rabbit neutrophil peptides (defensins).";
 RL Eur. J. Biochem. 216:653-659(1993).
 CC -!- FUNCTION: MICROBICIDAL ACTIVITY AND INHIBITS CORTICOTROPIN (ACTH)
 CC STIMULATED CORTICOSTERONE PRODUCTION.
 CC -!- TISSUE SPECIFICITY: LUNG, SPLEEN, SMALL INTESTINE, PITUITARY
 CC GLAND, ADRENAL MEDULLA AND PLASMA.
 CC -!- SIMILARITY: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.
 DR PIR; S36843; S36843.
 DR InterPro; IPR006081; Defensin_alpha.
 DR InterPro; IPR006080; Defensin_mammal.
 DR Pfam; PF00323; defensins; 1.
 DR SMART; SM00048; DEFSN; 1.
 DR PROSITE; PS00269; DEFENSIN; 1.
 KW Defensin; Antibiotic.
 FT DISULFID 3 31 BY SIMILARITY.
 FT DISULFID 5 20 BY SIMILARITY.
 FT DISULFID 10 30 BY SIMILARITY.
 SQ SEQUENCE 34 AA; 4052 MW; E0090709FA1512B9 CRC64;

Query Match 14.3%; Score 4; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRRF 16
 ||||
 Db 6 RRRF 9

RESULT 4

PAHO_MACMU
 ID PAHO_MACMU STANDARD; PRT; 36 AA.
 AC P33684;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Pancreatic hormone (Pancreatic polypeptide) (PP).
 GN PPY.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91164506; PubMed=2003150;
 RA Yu J., Xin Y., Eng J., Yalow R.S.;
 RT "Rhesus monkey gastroenteropancreatic hormones: relationship to human
 RT sequences.";
 RL Regul. Pept. 32:39-45(1991).

CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 CC GASTROINTESTINAL FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NPY family.
 DR PIR; C60071; C60071.
 DR HSSP; P01302; 1BBA.
 DR InterPro; IPR001955; Pancreatic_hormn.
 DR Pfam; PF00159; hormone3; 1.
 DR PRINTS; PR00278; PANCHORMONE.
 DR SMART; SM00309; PAH; 1.
 DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Pancreas; Amidation.
 FT MOD_RES 36 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4183 MW; 761B717671A7758F CRC64;

Query Match 14.3%; Score 4; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
 ||||
 Db 23 DLRR 26

RESULT 5

PAHO_RABIT

ID PAHO_RABIT STANDARD; PRT; 36 AA.
 AC P41336;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Pancreatic hormone (Pancreatic polypeptide) (PP).
 GN PPY.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=94130533; PubMed=8299350;
 RA Marks N.J., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "Rabbit pancreatic polypeptide."
 RL Comp. Biochem. Physiol. 106B:883-887(1993).
 CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 CC GASTROINTESTINAL FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NPY family.
 DR HSSP; P01302; 1BBA.
 DR InterPro; IPR001955; Pancreatic_hormn.
 DR Pfam; PF00159; hormone3; 1.
 DR PRINTS; PR00278; PANCHORMONE.
 DR SMART; SM00309; PAH; 1.
 DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.

DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation; Pancreas.
FT MOD_RES 36 36 AMIDATION.
SQ SEQUENCE 36 AA; 4197 MW; A14A4E0831A7759D CRC64;

Query Match 14.3%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
|||
Db 23 DLRR 26

RESULT 6

Y4KD_BPCHP

ID Y4KD_BPCHP STANDARD; PRT; 36 AA.

AC P19188;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE Hypothetical 4.7 kDa protein (ORF8).

OS Bacteriophage Chp1.

OC Viruses; ssDNA viruses; Microviridae; Microvirus.

OX NCBI_TaxID=12367;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90111716; PubMed=2607341;

RA Storey C.C., Lusher M., Richmond S.J.;

RT "Analysis of the complete nucleotide sequence of Chp1, a phage which

RT infects avian Chlamydia psittaci.";

RL J. Gen. Virol. 70:3381-3390(1989).

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DR EMBL; D00624; BAA00510.1; -.

KW Hypothetical protein.

SQ SEQUENCE 36 AA; 4670 MW; 98AF35E45B9545A4 CRC64;

Query Match 14.3%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRR 15
|||
Db 7 LRRR 10

RESULT 7

FIBA_CANFA

ID FIBA_CANFA STANDARD; PRT; 28 AA.

AC P02673; P14464;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Canis familiaris (Dog), and
 OS Vulpes vulpes (Red fox).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615, 9627;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.familiaris;
 RX MEDLINE=76081726; PubMed=1198547;
 RA Birken S., Wilner G.D., Canfield R.E.;
 RT "Studies of the structure of canine fibrinogen."
 RL Thromb. Res. 7:599-610(1975).
 RN [2]
 RP SEQUENCE OF 1-16.
 RC SPECIES=C.familiaris, and V.vulpes;
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals."
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [3]
 RP SEQUENCE OF 1-16.
 RC SPECIES=C.familiaris;
 RX MEDLINE=66020594; PubMed=5836555;
 RA Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
 RT "The nature of the peptides released from canine fibrinogen."
 RL Biochem. Biophys. Res. Commun. 14:555-558(1964).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR; A94308; A05296.
 KW Blood coagulation; Plasma; Phosphorylation.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT MOD_RES 3 3 PHOSPHORYLATION (PARTIAL).
 FT CONFLICT 2 2 N -> D (IN REF. 2).
 FT CONFLICT 4 7 KEGE -> EGKQ (IN REF. 2).
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2958 MW; 09DCD3F923BFEBD2 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 IAE 24
 |||
 Db 9 IAE 11

RESULT 8

GTS5_CHICK

ID GTS5_CHICK STANDARD; PRT; 28 AA.
 AC P20137;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Glutathione S-transferase 5 (EC 2.5.1.18) (GST-CL5) (GST class-sigma)
 DE (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90248419; PubMed=2337594;
 RA Chang L.-H., Chuang L.-F., Tsai C.-P., Tu C.-P.D., Tam M.F.;
 RT "Characterization of glutathione S-transferases from day-old chick
 RT livers.";
 RL Biochemistry 29:744-750(1990).
 CC -!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.
 DR PIR; C33948; C33948.
 DR InterPro; IPR004045; GST_Nterm.
 DR Pfam; PF02798; GST_N; 1.
 KW Transferase.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3389 MW; DA51DC0ABD203B12 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AEI 25
 |||
 Db 14 AEI 16

RESULT 9

HSP4_OCTVU

ID HSP4_OCTVU STANDARD; PRT; 28 AA.
 AC P83216;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm protamine P4 (Po4).
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=6645;

RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Sperm;
 RA Gimenez-Bonafe P., Ribes E., Buesa C., Sautiere P., Kouach M.,
 RA Ausio J., Kasinsky H.E., Chiva M.;
 RT "Chromatin remodelling and protamines during spermiogenesis of Octopus
 RT vulgaris (Cephalopoda).";
 RL J. Exp. Zool. 0:0-0(2001).
 CC !- FUNCTION: Protamines substitute for histones in the chromatin of
 CC sperm during the haploid phase of spermatogenesis. They compact
 CC sperm DNA into a highly condensed, stable and inactive
 CC complex.
 CC !- SUBCELLULAR LOCATION: Nuclear.
 CC !- TISSUE SPECIFICITY: Testis.
 CC !- MASS SPECTROMETRY: MW=3537; METHOD=Electrospray.
 DR GO; GO:0005718; C:nucleosome; NAS.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003677; F:DNA binding activity; NAS.
 DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; NAS.
 DR GO; GO:0007076; P:mitotic chromosome condensation; NAS.
 DR GO; GO:0006334; P:nucleosome assembly; NAS.
 DR GO; GO:0007283; P:spermatogenesis; NAS.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis;
 KW DNA-binding; DNA condensation; Nuclear protein.
 FT DOMAIN 1 7 POLY-ARG.
 FT DOMAIN 18 26 POLY-ARG.
 SQ SEQUENCE 28 AA; 3538 MW; A40B4D2C1B8E20ED CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
 |||
 Db 1 RRR 3

RESULT 10

PA23_TRIST
 ID PA23_TRIST STANDARD; PRT; 28 AA.
 AC P82894;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)
 DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
 OS Trimeresurus stejnegeri (Chinese green tree viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=39682;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Li S.Y., Wang W.Y., Xiong Y.L.;
 RT "Isolation, sequence and characterization of five variants of
 RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";

RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic
 CC activities are not detected.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
 CC SUBFAMILY.
 DR HSSP; P82287; 1QLL.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGK 7
 |||
 Db 5 LGK 7

RESULT 11

VG9_SPV4

ID VG9_SPV4 STANDARD; PRT; 28 AA.
 AC P11341;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-JUL-1989 (Rel. 11, Last annotation update)
 DE Gene 9 protein.
 GN 9.
 OS Spiroplasma virus 4 (SpV4).
 OC Viruses; ssDNA viruses; Microviridae; Spiromicrovirus.
 OX NCBI_TaxID=10855;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88032809; PubMed=2822658;
 RA Renaudin J., Pascarel M.-C., Bove J.-M.;
 RT "Spiroplasma virus 4: nucleotide sequence of the viral DNA,
 RT regulatory signals, and proposed genome organization.";
 RL J. Bacteriol. 169:4950-4961(1987).

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 CC -----

DR EMBL; M17988; -; NOT_ANNOTATED_CDS.
DR PIR; B29825; G9BPSV.
SQ SEQUENCE 28 AA; 3776 MW; 9916C3C9C3B9FD1D CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RRR 15
|||
Db 17 RRR 19

RESULT 12

VI03_VACCP

ID VI03_VACCP STANDARD; PRT; 28 AA.
AC Q00334;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Protein I3 (Fragment).
GN I3L.
OS Vaccinia virus (strain L-IVP).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=31531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91066899; PubMed=2250685;
RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
RA Malygin E.G.;
RT "Molecular-biological study of vaccinia virus genome. II.
RT Localization and nucleotide sequence of vaccinia virus genes coding
RT for proteins 36K and 12K.";
RL Mol. Biol. (Mosk) 24:968-976(1990).
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
CC THE LATE PHASE OF INFECTION.

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CC -----

DR EMBL; X61165; CAA43473.1; -.
DR InterPro; IPR006754; Pox_I3.
DR Pfam; PF04661; Pox_I3; 1.
KW Early protein; Late protein.
FT NON_TER 1 1
SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLG 6
|||
Db 5 NLG 7

RESULT 13

Y073_ARCFU

ID Y073_ARCFU STANDARD; PRT; 28 AA.
AC O30163;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0073.
GN AF0073.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
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CC -----
DR EMBL; AE001101; AAB91159.1; -.
DR PIR; A69259; A69259.
DR TIGR; AF0073; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 28 AA; 3222 MW; 4EA8550DA1345BC9 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AEI 25

Db

|||
17 AEI 19

RESULT 14

YA79_ARCFU

ID YA79_ARCFU STANDARD; PRT; 28 AA.

AC O29184;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein AF1079.

GN AF1079.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997).

CC -!- SIMILARITY: BELONGS TO THE UPF0165 FAMILY.

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CC -----

DR EMBL; AE001028; AAB90160.1; -.

DR PIR; G69384; G69384.

DR TIGR; AF1079; -.

DR InterPro; IPR002807; DUF104.

DR Pfam; PF01954; DUF104; 1.

DR ProDom; PD005964; DUF104_N; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 28 AA; 3289 MW; 22502C0A72E6A1D5 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLR 13
|||
Db 21 DLR 23

RESULT 15

12AH_CLOS4

ID 12AH_CLOS4 STANDARD; PRT; 29 AA.
AC P21215;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 12-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.176) (Fragment).
OS Clostridium sp. (strain C 48-50).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1507;
RN [1]
RP SEQUENCE.
RX MEDLINE=91177018; PubMed=2007406;
RA Braun M., Luensdorf H., Bueckmann A.F.;
RT "12 alpha-hydroxysteroid dehydrogenase from Clostridium group P,
RT strain C 48-50. Production, purification and characterization.";
RL Eur. J. Biochem. 196:439-450(1991).
CC -!- FUNCTION: Catalyzes the oxidation of the 12-alpha-hydroxyl group
CC of bile acids, both in their free and conjugated form. Also acts
CC on bile alcohols.
CC -!- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
CC cholanate + NADP(+) = 3-alpha,7-alpha-dihydroxy-12-oxo-5-beta-
CC cholanate + NADPH.
CC -!- SUBUNIT: Homotetramer.
CC -!- MISCELLANEOUS: The thermostability of the enzyme is greatly
CC increased due to NADP binding.
DR PIR; S14099; S14099.
KW Bile acid catabolism; Oxidoreductase; NADP.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2900 MW; A827DB34DB6C8812 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSI 9
|||
Db 17 KSI 19

RESULT 16

DMS5_PHYSA

ID DMS5_PHYSA STANDARD; PRT; 29 AA.
AC P80281;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 5 (DS V).
OS Phyllomedusa sauvagei (Sauvage's leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8395;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=94139686; PubMed=8306981;
 RA Mor A., Nicolas P.;
 RT "Isolation and structure of novel defensive peptides from frog skin."
 RL Eur. J. Biochem. 219:145-154(1994).
 CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
 CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
 CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Dermaseptin subfamily.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
 SQ SEQUENCE 29 AA; 2840 MW; 540A4971FC5BB506 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKS 8
 |||
 Db 10 GKS 12

RESULT 17

P2SM_LOXIN

ID P2SM_LOXIN STANDARD; PRT; 29 AA.
 AC P83046;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).
 OS Loxosceles intermedia (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
 OX NCBI_TaxID=58218;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR
 RP LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Venom;
 RX MEDLINE=99009277; PubMed=9790962;
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;
 RT "Sphingomyelinases in the venom of the spider Loxosceles intermedia
 RT are responsible for both dermonecrosis and complement-dependent
 RT hemolysis."
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-
 CC dependent hemolysis and dermonecrosis.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.

CC -!- COFACTOR: Calcium ion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 KW Hydrolase; Toxin; Calcium; Hemolysis.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLG 6
 |||
 Db 25 NLG 27

RESULT 18

PRO1_DACGL

ID PRO1_DACGL STANDARD; PRT; 29 AA.
 AC P18689;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Prolamin alpha-1 (Fragment).
 OS Dactylis glomerata (Orchard grass) (Cocksfoot grass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Dactylis.
 OX NCBI_TaxID=4509;
 RN [1]
 RP SEQUENCE.
 RA Vvedenskaya I.O., Shlyapnikov S.V., Konarev A.V.;
 RT "Characterization of the N-terminal amino acid sequence of alpha-
 RT prolamine from Dactylis glomerata L.";
 RL Biokhimiia 51:1519-1522(1986).
 DR PIR; S02200; S02200.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3647 MW; DEAE9B9ADC967D256 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 FFL 18
 |||
 Db 21 FFL 23

RESULT 19

CH60_CLOPA

ID CH60_CLOPA STANDARD; PRT; 30 AA.
 AC P81339;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (CP 3) (Fragment).
 GN GROL OR GROEL OR MOPA.

OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions (By similarity).
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chaprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3124 MW; 193F5EF05825BF1D CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSI 9
 |||
 Db 2 KSI 4

RESULT 20

HSP5_OCTVU

ID HSP5_OCTVU STANDARD; PRT; 30 AA.
 AC P83217;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm protamine P5 (Po5).
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=6645;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Sperm;
 RA Gimenez-Bonafe P., Ribes E., Buesa C., Sautiere P., Kouach M.,
 RA Ausio J., Kasinsky H.E., Chiva M.;
 RT "Chromatin remodelling and protamines during spermiogenesis of Octopus
 RT vulgaris (Cephalopoda).";
 RL J. Exp. Zool. 0:0-0(2001).
 CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
 CC sperm during the haploid phase of spermatogenesis. They compact

983	2	7.1	30	2	B45095	photosystem I ligh
984	2	7.1	30	2	A22977	delta-endotoxin -
985	2	7.1	30	2	S08565	ribulose-bisphosph
986	2	7.1	30	2	B61278	coat protein VP1 -
987	2	7.1	30	2	S30757	genome polyprotein
988	2	7.1	30	2	S30760	genome polyprotein
989	2	7.1	30	2	S30759	genome polyprotein
990	2	7.1	30	2	S13753	replication initia
991	2	7.1	30	2	S26175	tail tubular prote
992	2	7.1	30	2	S68312	glucuronosyltransf
993	2	7.1	30	2	S42364	aromatic-amino-aci
994	2	7.1	30	2	S05223	photosystem I 6.5K
995	2	7.1	30	2	S30333	N-carbamoyl-D-amin
996	2	7.1	30	2	S28991	antifungal protein
997	2	7.1	30	2	PC2307	X-Pro aminopeptida
998	2	7.1	30	2	PQ0484	globulin 1b - taro
999	2	7.1	30	2	C43591	51K outer membrane
1000	2	7.1	30	2	B56586	storage hexamer 2

ALIGNMENTS

RESULT 1

A05012

hypothetical protein 30 - liverwort (Marchantia polymorpha) chloroplast

C;Species: chloroplast Marchantia polymorpha

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 21-Jul-2000

C;Accession: S01582; A05012

R;Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Ohyama, K.; Ozeki, H.

J. Mol. Biol. 203, 299-331, 1988

A;Title: Structure and organization of Marchantia polymorpha chloroplast genome.

II. Gene organization of the large single copy region from rps'12 to atpB.

A;Reference number: S01567; MUID:89068686; PMID:2974085

A;Accession: S01582

A;Molecule type: DNA

A;Residues: 1-30 <UME>

A;Cross-references: EMBL:X04465; NID:g11640; PIDN:CAA28070.1; PID:g11657

A;Note: the authors translated the codon GAA for residue 2 as Val and ATT for residues 13 and 14 as Asn

R;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Aota, S.; Inokuchi, H.; Ozeki, H.

Nature 322, 572-574, 1986

A;Title: Chloroplast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA.

A;Reference number: A38014

A;Contents: annotation; gene organization, sites, features

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 14.3%; Score 4; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db ||||
 24 RFFL 27

RESULT 2

S34504

photosystem I protein psaM - *Euglena gracilis* chloroplast

C;Species: chloroplast *Euglena gracilis*

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999

C;Accession: S34504; S34871

R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.;

Spielmann, A.; Stutz, E.

submitted to the EMBL Data Library, January 1993

A;Description: The complete sequence of the *Euglena gracilis* chloroplast genome (tentative).

A;Reference number: S34494

A;Accession: S34504

A;Molecule type: DNA

A;Residues: 1-31 <HAL1>

A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50083.1; PID:g415739

R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.;

Spielmann, A.; Stutz, E.

Nucleic Acids Res. 21, 3537-3544, 1993

A;Title: Complete sequence of *Euglena gracilis* chloroplast DNA.

A;Reference number: S34862; MUID:93347989; PMID:8346031

A;Accession: S34871

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <HAL2>

A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50083.1; PID:g415739

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C;Genetics:

A;Gene: psaM

A;Genome: chloroplast

C;Superfamily: *Euglena gracilis* chloroplast photosystem I protein psaM

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 14.3%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGKS 8
 ||||
Db 25 LGKS 28

RESULT 3

PQ0416

RNA-directed RNA polymerase (EC 2.7.7.48) 3 - influenza A virus (strain

A/Yamagata/120/86 [H1N1]) (fragment)

N;Alternate names: P2 protein; PA protein

C;Species: influenza A virus

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PQ0416

R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo,

A.; Nerome, R.; Omoe, K.; Nerome, K.

J. Gen. Virol. 73, 1329-1337, 1992

A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H1N2) viruses isolated from man in China.

A;Reference number: PQ0408; MUID:92300326; PMID:1607856

A;Accession: PQ0416

A;Molecule type: genomic RNA

A;Residues: 1-33 <LIA>

C;Genetics:

A;Map position: segment 3

C;Superfamily: influenza virus RNA-directed RNA polymerase 3

C;Keywords: nucleotidyltransferase

Query Match 14.3%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSI 9
|||
Db 16 GKSI 19

RESULT 4

S36843

defensin NP-6 - rabbit

N;Contains: defensin des-G1-NP-6

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1998

C;Accession: S36843; S36844

R;Fuse, N.; Hayashi, Y.; Fukata, J.; Tominaga, T.; Ebisui, O.; Satoh, Y.;
Isohara, T.; Uno, I.; Imura, H.

Eur. J. Biochem. 216, 653-659, 1993

A;Title: Purification and characterization of new anti-adrenocorticotropin rabbit neutrophil peptides (defensins).

A;Reference number: S36843; MUID:93387318; PMID:8397087

A;Accession: S36843

A;Molecule type: protein

A;Residues: 1-34 <FUS>

A;Accession: S36844

A;Molecule type: protein

A;Residues: 2-34 <FU2>

A;Note: defensin des-G1-NP-6

C;Superfamily: mammalian defensin

Query Match 14.3%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRRF 16
|||
Db 6 RRRF 9

RESULT 5

A39888

synapsin I - rat (fragments)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 18-Jun-1993

C;Accession: A39888
R;Czernik, A.J.; Pang, D.T.; Greengard, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 7518-7522, 1987
A;Title: Amino acid sequences surrounding the cAMP-dependent and
calcium/calmodulin-dependent phosphorylation sites in rat and bovine synapsin I.
A;Reference number: A39888; MUID:88041137; PMID:3118371
A;Accession: A39888
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-34 <CZE>

Query Match 14.3%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRR 15
|||
Db 3 LRRR 6

RESULT 6

S20042

hypothetical protein 1 - Haemophilus influenzae insertion sequence IS1016(V-5)
(fragment)

C;Species: Haemophilus influenzae

C;Date: 07-May-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

C;Accession: S20042

R;Kroll, J.S.; Loynds, B.M.; Moxon, E.R.

Mol. Microbiol. 5, 1549-1560, 1991

A;Title: The Haemophilus influenzae capsulation gene cluster: a compound
transposon.

A;Reference number: S16288; MUID:92157882; PMID:1664907

A;Accession: S20042

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-35 <KRO>

A;Cross-references: EMBL:X58177

C;Genetics:

A;Mobile element: insertion sequence IS1016(V-5)

Query Match 14.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSIQ 10
|||
Db 10 KSIQ 13

RESULT 7

E64108

protein V6, truncated - Haemophilus influenzae insertion sequence IS1016

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1998

C;Accession: E64108

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;

Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.;

McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: E64108

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-35 <TIGR>

A;Cross-references: GB:U32782; GB:L42023; NID:g1574041; PID:g1574052;

TIGR:HI1018

A;Experimental source: strain Rd KW20

C;Genetics:

A;Mobile element: insertion sequence IS1016

Query Match 14.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSIQ 10
|||
Db 10 KSIQ 13

RESULT 8

D82607

hypothetical protein XF2026 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: D82607

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil.

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: D82607

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <SIM>

A;Cross-references: GB:AE004021; GB:AE003849; NID:g9107139; PIDN:AAF84828.1;

GSPDB:GN00128; XFSC:XF2026

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Alves, L.M.C.; Araya, J.E.; Baia, G.S.; Baptista, C.S.; Barros, M.H.; Bonaccorsi, E.D.; Bordin, S.; Bove, J.M.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Colauto, N.B.; Colombo, C.; Costa, F.F.; Costa, M.C.R.; Costa-Neto, C.M.; Coutinho, L.L.; Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme, M.; Furlan, L.R.; Garnier, M.; Goldman, G.H.; Goldman, M.H.S.; Gomes, S.L.; Gruber, A.; Ho, P.L.; Hoheisel, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, F.; Lambais, M.R.; Leite, L.C.C.; Lemos, E.G.M.; Lemos, M.V.F.; Lopes, S.A.; Lopes, C.R.; Machado, J.A.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.L.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Monteiro-Vitorello, C.B.; Moon, D.H.; Nagai, M.A.; Nascimento, A.L.T.O.; Netto, L.E.S.; Nhani Jr., A.; Nobrega, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Paris, A.; Peixoto, B.R.; Pereira, G.A.G.; Pereira Jr., H.A.; Pesquero, J.B.; Quaggio, R.B.; Roberto, P.G.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, H.E.

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza, A.P.; Terenzi, M.F.; Truffi, D.; Tsai, S.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zago, M.A.; Zatz, M.; Meidanis, J.; Setubal, J.C.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF2026

Query Match 14.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIAE 24
|||
Db 30 LIAE 33

RESULT 9

JU0352

4.6K protein - Chlamydophila psittaci phage Chp1

C;Species: Chlamydophila psittaci phage Chp1, Chlamydia psittaci phage Chp1

A;Note: host Chlamydia psittaci

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000

C;Accession: JU0352

R;Storey, C.C.; Lusher, M.; Richmond, S.J.

J. Gen. Virol. 70, 3381-3390, 1989

A;Title: Analysis of the complete nucleotide sequence of Chp1, a phage which infects avian Chlamydia psittaci.

A;Reference number: JU0345; MUID:90111716; PMID:2607341

A;Accession: JU0352

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:D00624; NID:g217761; PIDN:BAA00510.1; PID:g217769

C;Superfamily: Chlamydia psittaci phage Chp1 4.6K protein

Query Match 14.3%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRR 15
|||

Db 7 LRRR 10

RESULT 10

C60071

pancreatic hormone - rhesus macaque

N;Alternate names: pancreatic polypeptide

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 15-Jun-1996

C;Accession: C60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: C60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-36 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: pancreatic hormone

C;Keywords: amidated carboxyl end; hormone; pancreas

F;36/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 14.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
|||
Db 23 DLRR 26

RESULT 11

S17507

cytokine - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C;Accession: S17507

R;Jose, P.J.; Collins, P.D.; Perkins, J.A.; Beaubien, B.C.; Totty, N.F.;

Waterfield, M.D.; Hsuan, J.; Williams, T.J.

Biochem. J. 278, 493-497, 1991

A;Title: Identification of a second neutrophil-chemoattractant cytokine generated during an inflammatory reaction in the rabbit peritoneal cavity in vivo. Purification, partial amino acid sequence and structural relationship to melanoma-growth-stimulatory activity.

A;Reference number: S17507; MUID:91378900; PMID:1898341

A;Accession: S17507

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-36 <JOS>

C;Superfamily: beta-thromboglobulin

Query Match 14.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSIQ 10
 ||||
Db 19 KSIQ 22

RESULT 12

S04627

glutathione transferase (EC 2.5.1.18) 6.0 - *Proteus mirabilis* (fragment)

C;Species: *Proteus mirabilis*

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 01-Feb-1999

C;Accession: S04627

R;Di Ilio, C.; Aceto, A.; Piccolomini, R.; Allocati, N.; Caccuri, A.M.; Barra, D.; Federici, G.

FEBS Lett. 250, 57-59, 1989

A;Title: N-terminal region of *Proteus mirabilis* glutathione transferase is not homologous to mammalian and plant glutathione transferases.

A;Reference number: S04627; MUID:89290034; PMID:2661269

A;Accession: S04627

A;Molecule type: protein

A;Residues: 1-38 <DII>

C;Complex: dimer

C;Function:

A;Description: catalyzes conjugation of glutathione to a large variety of electrophilic compounds of endobiotic and xenobiotic origin; also involved in intracellular binding and transport of hydrophobic compounds; involved in detoxification of organic hydroperoxides

C;Superfamily: glutathione transferase

C;Keywords: dimer; transferase

Query Match 14.3%; Score 4; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLRR 14
 ||||
Db 31 DLRR 34

RESULT 13

B39888

synapsin I - bovine (fragments)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 18-Jun-1993

C;Accession: B39888

R;Czernik, A.J.; Pang, D.T.; Greengard, P.

Proc. Natl. Acad. Sci. U.S.A. 84, 7518-7522, 1987

A;Title: Amino acid sequences surrounding the cAMP-dependent and calcium/calmodulin-dependent phosphorylation sites in rat and bovine synapsin I.

A;Reference number: A39888; MUID:88041137; PMID:3118371

A;Accession: B39888

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-38 <CZE>

Query Match 14.3%; Score 4; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRRR 15
|||
Db 3 LRRR 6

RESULT 14

A38335

58K tubulointerstitial nephritis antigen - rabbit (fragments)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 28-Jun-1991 #sequence_revision 24-Feb-1994 #text_change 24-Feb-1994

C;Accession: A38335; B38335

R;Butkowski, R.J.; Langeveld, J.P.M.; Wieslander, J.; Brentjens, J.R.; Andres, G.A.

J. Biol. Chem. 265, 21091-21098, 1990

A;Title: Characterization of a tubular basement membrane component reactive with autoantibodies associated with tubulointerstitial nephritis.

A;Reference number: A38335; MUID:91065920; PMID:2250013

A;Accession: A38335

A;Molecule type: protein

A;Residues: 1-38 <BUT>

A;Note: the source of this sequence is the 58K antigen

A;Accession: B38335

A;Molecule type: protein

A;Residues: 1-12 <BU2>

A;Note: the source of this sequence is the 50K antigen

Query Match 14.3%; Score 4; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 IAEI 25
|||
Db 26 IAEI 29

RESULT 15

E86077

hypothetical protein Z5430 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)

C;Species: *Escherichia coli*

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: E86077

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamiosis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: E86077

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-38 <STO>

A;Cross-references: GB:AE005174; NID:g12518780; PIDN:AAG59081.1; GSPDB:GN00145; UWGP:Z5430

A;Experimental source: strain 0157:H7, substrain EDL933

C;Genetics:

A;Gene: Z5430

Query Match 14.3%; Score 4; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHNL 5
||||
Db 20 LHNL 23

RESULT 16

S67938

hypothetical protein 3 - Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae

C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S67938

R;Saluja, S.K.; Weiser, J.N.

Mol. Microbiol. 16, 215-227, 1995

A;Title: The genetic basis of colony opacity in Streptococcus pneumoniae:
evidence for the effect of box elements on the frequency of phenotypic
variation.

A;Reference number: S67936; MUID:96015435; PMID:7565084

A;Accession: S67938

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-39 <SAL>

A;Cross-references: EMBL:U12567

Query Match 14.3%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGKS 8
||||
Db 5 LGKS 8

RESULT 17

G9BPSV

gene 9 protein - spiroplasma virus 4

C;Species: spiroplasma virus 4, SpV4

A;Note: host Spiroplasma melliferum

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 07-Dec-1999

C;Accession: B29825

R;Renaudin, J.; Pascarel, M.C.; Bove, J.M.

J. Bacteriol. 169, 4950-4961, 1987

A;Title: Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory
signals, and proposed genome organization.

A;Reference number: A91845; MUID:88032809; PMID:2822658

A;Accession: B29825

A;Molecule type: DNA

A;Residues: 1-28 <REN>

A;Cross-references: GB:M17988; NID:g334998

A;Note: this ORF is not annotated in GenBank entry SPVDNA

C;Comment: This virus is a procaryote DNA virus.
C;Genetics:
A;Gene: 9
A;Genetic code: SGC3
C;Superfamily: spiroplasma virus 4 gene 9 protein

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
|||
Db 17 RRR 19

RESULT 18

S41774

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Trypanosoma congolense mitochondrion (fragment)

C;Species: mitochondrion Trypanosoma congolense

C;Date: 25-Dec-1994 #sequence_revision 27-Feb-1997 #text_change 03-Jun-2002

C;Accession: S41774

R;Read, L.K.; Fish, W.R.; Muthiani, A.M.; Stuart, K.

Nucleic Acids Res. 21, 4073-4078, 1993

A;Title: Maxicircle DNA and edited mRNA sequences of closely related trypanosome species: implications of kRNA editing for evolution of maxicircle genomes.

A;Reference number: S41774; MUID:93382785; PMID:8396763

A;Accession: S41774

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-28 <REA>

C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol-plastocyanin reductase 17K protein homology

C;Keywords: electron transfer; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; RNA editing

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 FFL 18
|||
Db 9 FFL 11

RESULT 19

S66436

allophycocyanin alpha-B chain - Anabaena sp. (strain PCC 7120) (fragment)

C;Species: Anabaena sp.

A;Variety: PCC 7120

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 24-Oct-1997

C;Accession: S66436

R;Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.

Eur. J. Biochem. 236, 1010-1024, 1996

A;Title: Isolation, characterization and electron microscopy analysis of a hemidiscoidal phycobilisome type from the cyanobacterium Anabaena sp. PCC 7120.

A;Reference number: S66435; MUID:96270757; PMID:8665889

A;Accession: S66436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DUC>
C;Superfamily: phycocyanin

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSI 9
|||
Db 23 KSI 25

RESULT 20

C33948

glutathione transferase (EC 2.5.1.18) 5 - chicken (fragment)

N;Alternate names: glutathione S-alkyltransferase; glutathione S-aralkyltransferase; glutathione S-aryltransferase

C;Species: Gallus gallus (chicken)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 03-Nov-2000

C;Accession: C33948

R;Chang, L.H.; Chuang, L.F.; Tsai, C.P.; Tu, C.P.D.; Tam, M.F.

Biochemistry 29, 744-750, 1990

A;Title: Characterization of glutathione S-transferases from day-old chick livers.

A;Reference number: A90547; MUID:90248419; PMID:2337594

A;Accession: C33948

A;Molecule type: protein

A;Residues: 1-28 <CH3>

C;Superfamily: glutathione transferase

C;Keywords: transferase

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AEI 25
|||
Db 14 AEI 16

RESULT 21

A31859

deoxycytidine kinase (EC 2.7.1.74) / deoxyadenosine kinase (EC 2.7.1.76) - Lactobacillus acidophilus (fragment)

C;Species: Lactobacillus acidophilus

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 18-Sep-1998

C;Accession: A31859

R;Ikeda, S.; Swenson, R.P.; Ives, D.H.

Biochemistry 27, 8648-8652, 1988

A;Title: Amino-terminal nucleotide-binding sequences of a Lactobacillus deoxynucleoside kinase complex isolated by novel affinity chromatography.

A;Reference number: A31859; MUID:89118283; PMID:2851331

A;Accession: A31859

A;Molecule type: protein

A;Residues: 1-28 <IKE>
A;Note: 18-Ile, 21-Lys, 26-Gln, and 27-Ala were also found
C;Superfamily: Lactobacillus acidophilus deoxyadenosine kinase
C;Keywords: phosphotransferase

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKS 8
|||
Db 11 GKS 13

RESULT 22

B54257

deoxynucleoside kinase complex I F-component - Lactobacillus acidophilus
(fragment)

N;Alternate names: dCyd kinase subunit

C;Species: Lactobacillus acidophilus

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Sep-1998

C;Accession: B54257

R;Ikeda, S.; Ma, G.T.; Ives, D.H.

Biochemistry 33, 5328-5334, 1994

A;Title: Heterodimeric deoxynucleoside kinases of Lactobacillus acidophilus R-26: functional assignment of subunits using limited proteolysis controlled by end-product inhibitors.

A;Reference number: A54257; MUID:94227067; PMID:8172906

A;Accession: B54257

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <IKE>

A;Experimental source: R-26

A;Note: sequence extracted from NCBI backbone (NCBIP:146749)

C;Superfamily: Lactobacillus acidophilus deoxyadenosine kinase

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKS 8
|||
Db 11 GKS 13

RESULT 23

D41912

T-cell receptor beta chain (AE16) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C;Accession: D41912

R;Hong, S.C.; Chelouche, A.; Lin, R.; Shaywitz, D.; Braunstein, N.S.; Glimcher, L.; Janeway Jr., C.A.

Cell 69, 999-1009, 1992

A;Title: An MHC interaction site maps to the amino-terminal half of the T cell receptor alpha chain variable domain.

A;Reference number: A41912; MUID:92298397; PMID:1318787

A;Accession: D41912
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-28 <HON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLR 13
|||
Db 25 DLR 27

RESULT 24

I50169

alpha-1 type-1 collagen - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999

C;Accession: I50169

R;Yamada, Y.; Mudryj, M.; de Crombrughe, B.

J. Biol. Chem. 258, 14914-14919, 1983

A;Title: A uniquely conserved regulatory signal is found around the translation initiation site in three different collagen genes.

A;Reference number: I50169; MUID:84087884; PMID:6689169

A;Accession: I50169

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <YAM>

A;Cross-references: GB:K01482; NID:g211287; PIDN:AAA48636.1; PID:g555426

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIA 23
|||
Db 12 LIA 14

RESULT 25

S21231

calcium-binding protein SCP VI, sarcoplasmic - common lancelet

C;Species: Branchiostoma lanceolatum (common lancelet)

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C;Accession: S21231

R;Takagi, T.; Valette-Talbi, L.; Cox, J.A.

FEBS Lett. 302, 159-160, 1992

A;Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-binding proteins.

A;Reference number: S21153; MUID:92339504; PMID:1633848

A;Accession: S21231

A;Molecule type: protein

A;Residues: 1-28 <TAK>
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; EF hand

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 FFL 18
|||
Db 5 FFL 7

RESULT 26

A05296

fibrinogen alpha chain - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996

C;Accession: A94308; A03118; A37511; A05296; B37511; C03118

R;Birken, S.; Wilner, G.D.; Canfield, R.E.

Thromb. Res. 7, 599-610, 1975

A;Title: Studies of the structure of canine fibrinogen.

A;Reference number: A94308; MUID:76081726; PMID:1198547

A;Accession: A94308

A;Molecule type: protein

A;Residues: 1-28 <BIR>

R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.

Acta Chem. Scand. 19, 1789-1791, 1965

A;Title: Studies on fibrinopeptides from mammals.

A;Reference number: A03118

A;Accession: A03118

A;Molecule type: protein

A;Residues: 1-16 <BLO>

R;Osbaahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.

Biochem. Biophys. Res. Commun. 14, 555-558, 1964

A;Reference number: A37511; MUID:66020594; PMID:5836555

A;Accession: A37511

A;Molecule type: protein

A;Residues: 1,'D',3,'EGKQ',8-16 <OSB>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

C;Keywords: blood coagulation; liver; phosphoprotein; plasma

F;1-16/Product: fibrinopeptide A #status experimental <APT>

F;3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 IAE 24
|||
Db 9 IAE 11

RESULT 27

B35577

cell adhesion receptor CD36 - bovine (fragment)

N;Alternate names: membrane glycoprotein PAS IV; platelet glycoprotein IV

C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Sep-1990 #sequence_revision 10-May-1996 #text_change 29-Aug-1997
 C;Accession: B35577; A37884
 R;Greenwalt, D.E.; Watt, K.W.K.; So, O.Y.; Jiwani, N.
 Biochemistry 29, 7054-7059, 1990
 A;Title: PAS IV, an integral membrane protein of mammary epithelial cells, is related to platelet and endothelial cell CD36 (GP IV).
 A;Reference number: A35577; MUID:91027734; PMID:1699598
 A;Accession: B35577
 A;Molecule type: protein
 A;Residues: 1-28 <GRE>
 R;Greenwalt, D.E.; Watt, K.W.K.; Hasler, T.; Howard, R.J.; Patel, S.
 J. Biol. Chem. 265, 16296-16299, 1990
 A;Title: Structural, functional, and antigenic differences between bovine heart endothelial CD36 and human platelet CD36.
 A;Reference number: A37884; MUID:90375491; PMID:1697855
 A;Accession: A37884
 A;Molecule type: protein
 A;Residues: 1-21 <GR2>
 C;Superfamily: lysosomal integral membrane protein II
 C;Keywords: cell adhesion; glycoprotein; receptor; surface antigen; transmembrane protein

Query Match 10.7%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIA 23
 |||
 Db 8 LIA 10

RESULT 28

PN0047

signal transduction protein QM0017 - mouse (fragments)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 15-Oct-1999

C;Accession: PN0047

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0047

A;Molecule type: protein

A;Residues: 1-28 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.

C;Superfamily: signal transduction protein DJ-1

C;Keywords: brain

Query Match 10.7%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NLG 6

Db |||
 14 NLG 16

RESULT 29

I48178

orphan receptor - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48178

R;Pena de Ortiz, S.; Cannon, M.M.; Jamieson, G.A.

Brain Res. Mol. Brain Res. 23, 278-283, 1994

A;Title: Expression of nuclear hormone receptors within the rat hippocampus: identification of novel orphan receptors.

A;Reference number: I48178; MUID:94335560; PMID:7914660

A;Accession: I48178

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:L19344; NID:g349093; PIDN:AAB46396.1; PID:g565378

C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SIQ 10
 |||
Db 6 SIQ 8

RESULT 30

B56779

tetM 5'-region leader peptide - Enterococcus faecalis transposon Tn916

C;Species: Enterococcus faecalis

C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 24-Sep-1999

C;Accession: B56779

R;Su, Y.A.; He, P.; Clewell, D.B.

Antimicrob. Agents Chemother. 36, 769-778, 1992

A;Title: Characterization of the tet(M) determinant of Tn916: evidence for regulation by transcription attenuation.

A;Reference number: A56779; MUID:92368175; PMID:1323953

A;Accession: B56779

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <SU1>

A;Cross-references: GB:U09422; NID:g532533; PIDN:AAB60021.1; PID:g532545

A;Note: sequence extracted from NCBI backbone (NCBIN:111076, NCBIP:111079)

C;Superfamily: unassigned leader peptides

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSI 9
 |||

Db 15 KSI 17

RESULT 31

G69384

conserved hypothetical protein AF1079 - *Archaeoglobus fulgidus*

C;Species: *Archaeoglobus fulgidus*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C;Accession: G69384

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69384

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-28 <KLE>

A;Cross-references: GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB90160.1;

PID:g2649506; TIGR:AF1079

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLR 13
|||
Db 21 DLR 23

RESULT 32

A69259

hypothetical protein AF0073 - *Archaeoglobus fulgidus*

C;Species: *Archaeoglobus fulgidus*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C;Accession: A69259

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69259
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <KLE>
A;Cross-references: GB:AE001101; GB:AE000782; NID:g2689424; PIDN:AAB91159.1; PID:g2650579; TIGR:AF0073

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AEI 25
|||
Db 17 AEI 19

RESULT 33

T14905

hypothetical protein - parsley

C;Species: *Petroselinum crispum* (parsley)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T14905

R;Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.;
Weisshaar, B.

Plant Cell 6, 1607-1621, 1994

A;Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.

A;Reference number: Z18259; MUID:95128172; PMID:7827494

A;Accession: T14905

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <FEL>

A;Cross-references: EMBL:S75395; NID:g913201; PID:e194726

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLH 3
|||
Db 14 LLH 16

RESULT 34

JQ0272

hypothetical 3K protein (trnH-trnV intergenic region) - rice chloroplast

C;Species: chloroplast *Oryza sativa* (rice)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jul-2000

C;Accession: JQ0272; S05152

R;Shimada, H.; Whittier, R.F.; Hiratsuka, J.; Maeda, Y.; Hirai, A.; Sugiura, M.
submitted to JIPID, December 1989

A;Reference number: JQ0200

A;Accession: JQ0272

A;Molecule type: DNA

A;Residues: 1-28 <SHI>
 A;Experimental source: cv. Nihonbare
 R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kondo, C.; Honji, Y.; Sun, C.R.; Meng, B.Y.; Li, Y.Q.; Kanno, A.; Nishizawa, Y.; Hirai, A.; Shinozaki, K.; Sugiura, M.
 Mol. Gen. Genet. 217, 185-194, 1989
 A;Title: The complete sequence of the rice (*Oryza sativa*) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.
 A;Reference number: S05080; MUID:89364698; PMID:2770692
 A;Accession: S05152
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-28 <HIR>
 A;Cross-references: GB:X15901; NID:g11957; PIDN:CAA33939.1; PID:g12032
 A;Note: this sequence was submitted to EMBL, July 1989
 C;Genetics:
 A;Genome: chloroplast
 C;Keywords: chloroplast

Query Match 10.7%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 HHL 21
 |||
 Db 19 HHL 21

RESULT 35

S07826
 venom protein - American tarantula (*Eurypelma californica*) (fragment)
 C;Species: *Eurypelma californica*
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C;Accession: S07826
 R;Savel-Niemann, A.
 Biol. Chem. Hoppe-Seyler 370, 485-498, 1989
 A;Title: Tarantula (*Eurypelma californicum*) venom, a multicomponent system.
 A;Reference number: S04224; MUID:89302691; PMID:2742756
 A;Accession: S07826
 A;Molecule type: protein
 A;Residues: 1-28 <SAV>
 C;Keywords: venom

Query Match 10.7%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKS 8
 |||
 Db 20 GKS 22

RESULT 36

I54183
 cell adhesion regulator - human (fragment)
 C;Species: *Homo sapiens* (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C;Accession: I54183
R;Koyama, K.; Emi, M.; Nakamura, Y.
Genomics 16, 264-265, 1993
A;Title: The cell adhesion regulator (CAR) gene; TaqI and insertion/deletion polymorphism, and regional assignment to the peritelomeric region of 16q by linkage analysis.
A;Reference number: I54183; MUID:93252394; PMID:8098008
A;Accession: I54183
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: GB:D14075; NID:g219525; PIDN:BAA03160.1; PID:g219526

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRR 14
|||
Db 14 LRR 16

RESULT 37

JQ1035
hypothetical 3.2K protein (type I IGFR 5' region) - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: JQ1035
R;Cooke, D.W.; Bankert, L.A.; Roberts Jr., C.T.; LeRoith, D.; Casella, S.J.
Biochem. Biophys. Res. Commun. 177, 1113-1120, 1991
A;Title: Analysis of the human type I insulin-like growth factor receptor promotor region.
A;Reference number: PQ0159; MUID:91282751; PMID:1711844
A;Accession: JQ1035
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <COO>

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRR 14
|||
Db 18 LRR 20

RESULT 38

S51593
myrB protein - Micromonospora griseorubida (fragment)
C;Species: Micromonospora griseorubida
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C;Accession: S51593
R;Inouye, M.; Takada, Y.; Muto, N.; Beppu, T.; Horinouchi, S.
Mol. Gen. Genet. 245, 456-464, 1994

A;Title: Characterization and expression of a P-450-like mycinamicin biosynthesis gene using a novel Micromonospora-Escherichia coli shuttle cosmid vector.

A;Reference number: S51593; MUID:95107242; PMID:7808395

A;Accession: S51593

A;Molecule type: DNA

A;Residues: 1-28 <INO>

A;Cross-references: EMBL:D16098; NID:g286050; PIDN:BAA03671.1; PID:d1004186; PID:g829046

C;Genetics:

A;Gene: myrB

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
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Db 22 RRR 24

RESULT 39

JN0014

GABA(A) receptor alpha-1 chain /glycine receptor alpha-1 chain engineered fusion protein - synthetic (fragment)

C;Species: synthetic

A;Note: Rattus norvegicus (Norway rat) gene 5' region with engineered signal sequence derived from GABA(A) receptor

C;Date: 31-Mar-1990 #sequence_revision 30-Apr-1998 #text_change 13-Aug-1999

C;Accession: JN0014

R;Sontheimer, H.; Becker, C.M.; Pritchett, D.B.; Schofield, P.R.; Grenningloh, G.; Kettenmann, H.; Betz, H.; Seeburg, P.H.

Neuron 2, 1491-1497, 1989

A;Title: Functional chloride channels by mammalian cell expression of rat glycine receptor subunit.

A;Reference number: JN0014; MUID:90180468; PMID:2483325

A;Accession: JN0014

A;Molecule type: mRNA

A;Residues: 1-28 <SON>

C;Comment: See PIR:S20662.

F;1-20/Region: GABA(A) receptor alpha-1 chain-derived

F;21-28/Region: glycine receptor alpha-1 chain-derived

Query Match 10.7%; Score 3; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKS 8
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Db 2 GKS 4

RESULT 40

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527
 R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;
 Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.
 J. Bacteriol. 176, 1746-1755, 1994
 A;Title: Isolation, phenotypic characterization, and complementation analysis of
 mutants of *Methylobacterium extorquens* AM1 unable to synthesize pyrroloquinoline
 quinone and sequences of pqqD, pqqG, and pqqC.
 A;Reference number: A55527; MUID:94179111; PMID:8132470
 A;Accession: A55527
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-29 <MOR>
 A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
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 A;Gene: pqqD
 C;Superfamily: pyrroloquinoline quinone precursor pqqA
 C;Keywords: quinoprotein
 F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
 F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 10.7%; Score 3; DB 1; Length 29;
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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AEI 25
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 Db 23 AEI 25

Search completed: January 14, 2004, 10:37:32
 Job time : 11.2866 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 18.8411 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-169
Perfect score: 28
Sequence: 1 LLHNLGKSIQDLRRRFFLHHLIAEIHTA 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	23	82.1	28	11	US-09-843-221A-68	Sequence 68, Appl
4	23	82.1	34	9	US-09-169-786-5	Sequence 5, Appli
5	23	82.1	34	10	US-09-423-800-75	Sequence 75, Appl
6	23	82.1	34	11	US-09-843-221A-63	Sequence 63, Appl
7	23	82.1	34	12	US-10-337-981-75	Sequence 75, Appl
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9	23	82.1	34	14	US-10-097-079-2	Sequence 2, Appli
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219	5	17.9	34	11	US-09-843-221A-90	Sequence 90, Appl
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222	5	17.9	34	11	US-09-843-221A-122	Sequence 122, App
223	5	17.9	34	11	US-09-843-221A-123	Sequence 123, App
224	5	17.9	34	11	US-09-843-221A-128	Sequence 128, App
225	5	17.9	34	11	US-09-843-221A-161	Sequence 161, App
226	5	17.9	34	11	US-09-843-221A-164	Sequence 164, App
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230	5	17.9	34	12	US-10-361-928-5	Sequence 5, Appli
231	5	17.9	34	12	US-10-361-928-8	Sequence 8, Appli
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235	5	17.9	34	12	US-10-340-484-16	Sequence 16, Appl
236	5	17.9	34	12	US-10-340-484-17	Sequence 17, Appl
237	5	17.9	34	12	US-10-340-484-18	Sequence 18, Appl
238	5	17.9	34	12	US-10-340-484-19	Sequence 19, Appl
239	5	17.9	34	12	US-10-340-484-20	Sequence 20, Appl
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241	5	17.9	34	12	US-10-340-484-23	Sequence 23, Appl
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243	5	17.9	34	14	US-10-016-403-6	Sequence 6, Appli
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269	4	14.3	29	12	US-10-351-641-596	Sequence 596, App
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274	4	14.3	29	15	US-10-092-750-45	Sequence 45, Appl
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276	4	14.3	29	15	US-10-091-504-638	Sequence 638, App
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317	4	14.3	32	15	US-10-174-410-243	Sequence 243, App
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327	4	14.3	33	12	US-10-351-641-594	Sequence 594, App
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363	4	14.3	35	12	US-10-351-641-115	Sequence 115, App
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366	4	14.3	35	12	US-10-351-641-681	Sequence 681, App
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368	4	14.3	35	12	US-10-351-641-684	Sequence 684, App
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373	4	14.3	35	12	US-10-351-641-706	Sequence 706, App
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376	4	14.3	35	12	US-10-351-641-709	Sequence 709, App
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381	4	14.3	35	12	US-10-351-641-714	Sequence 714, App
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392	4	14.3	35	12	US-10-351-641-833	Sequence 833, App
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422	4	14.3	37	8	US-08-851-965-25	Sequence 25, Appl
423	4	14.3	37	8	US-08-851-965-26	Sequence 26, Appl
424	4	14.3	37	8	US-08-851-965-27	Sequence 27, Appl
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447	4	14.3	38	12	US-10-264-049-3208	Sequence 3208, Ap
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781	3	10.7	29	12	US-10-189-437-306	Sequence 306, App
782	3	10.7	29	12	US-10-189-437-693	Sequence 693, App
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786	3	10.7	29	12	US-09-820-649-286	Sequence 286, App
787	3	10.7	29	12	US-10-231-889-44	Sequence 44, Appl
788	3	10.7	29	12	US-09-818-683-308	Sequence 308, App
789	3	10.7	29	12	US-09-818-683-581	Sequence 581, App
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804	3	10.7	29	14	US-10-001-876-168	Sequence 168, App
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818	3	10.7	29	15	US-10-226-956-305	Sequence 305, App
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953	3	10.7	30	12	US-09-933-767-768	Sequence 768, App
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969	3	10.7	30	12	US-09-818-683-321	Sequence 321, App
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984	3	10.7	30	14	US-10-115-695-33	Sequence 33, Appl
985	3	10.7	30	14	US-10-078-059-23	Sequence 23, Appl
986	3	10.7	30	14	US-10-108-929-4	Sequence 4, Appli
987	3	10.7	30	15	US-10-006-069A-217	Sequence 217, App
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991	3	10.7	30	15	US-10-091-572-389	Sequence 389, App
992	3	10.7	30	15	US-10-091-244A-12	Sequence 12, Appl
993	3	10.7	30	15	US-10-143-090-268	Sequence 268, App
994	3	10.7	30	15	US-10-227-629-14	Sequence 14, Appl
995	3	10.7	30	15	US-10-051-841-5	Sequence 5, Appli
996	3	10.7	30	15	US-10-059-261-55	Sequence 55, Appl
997	3	10.7	30	15	US-10-059-261-163	Sequence 163, App
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ALIGNMENTS

RESULT 1

US-09-843-221A-69

; Sequence 69, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTHrP
US-09-843-221A-69

Query Match 100.0%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLHNLGKSIQDLRRRFFLHHLIAEIHTA 28
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Db 1 LLHNLGKSIQDLRRRFFLHHLIAEIHTA 28

RESULT 2

US-09-843-221A-169

; Sequence 169, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTHrP
; NAME/KEY: misc_feature
; LOCATION: (28)..(28)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-169

Query Match 100.0%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-843-221A-68
; Sequence 68, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-68

Query Match 82.1%; Score 23; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 GKSIQDLRRRFFLHHLIAEIHTA 28

RESULT 4

US-09-169-786-5
; Sequence 5, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 34

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-5

Query Match 82.1%; Score 23; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 5

US-09-423-800-75
; Sequence 75, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-75

Query Match 82.1%; Score 23; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 6

US-09-843-221A-63
; Sequence 63, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-63

Query Match 82.1%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
|||
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 7

US-10-337-981-75
; Sequence 75, Application US/10337981
; Publication No. US20030138424A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/10/337,981
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-981-75

Query Match 82.1%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      6 GKSIQDLRRRFFLHHLIAEIHTA 28
          |||||
Db      12 GKSIQDLRRRFFLHHLIAEIHTA 34
```

RESULT 8

US-10-340-484-21

; Sequence 21, Application US/10340484

; Publication No. US20030171288A1

; GENERAL INFORMATION:

; APPLICANT: Stewart, Andrew F.

; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic

; TITLE OF INVENTION: Drugs

; FILE REFERENCE: 25200-501

; CURRENT APPLICATION NUMBER: US/10/340,484

; CURRENT FILING DATE: 2003-01-10

; PRIOR APPLICATION NUMBER: 60/347,215

; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: 60/353,296

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/368,955

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: 60/379,125

; PRIOR FILING DATE: 2002-05-08

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Felis catus

US-10-340-484-21

Query Match 82.1%; Score 23; DB 12; Length 34;

Best Local Similarity 100.0%; Pred. No. 7e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      6 GKSIQDLRRRFFLHHLIAEIHTA 28
          |||||
Db      12 GKSIQDLRRRFFLHHLIAEIHTA 34
```

RESULT 9

US-10-097-079-2

; Sequence 2, Application US/10097079

; Publication No. US20020132973A1

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.

; Morize, Isabelle

; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3C43

; CITY: Collegeville

; STATE: PA

```

; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: No. US20020132973A1 Relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-097-079-2

```

```

Query Match          82.1%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 GKSIQDLRRRFFLHHLIAEIHTA 28
        |||||
Db      12 GKSIQDLRRRFFLHHLIAEIHTA 34

```

RESULT 10

US-10-182-018-75

```

; Sequence 75, Application US/10182018
; Publication No. US20030049211A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
; FILE REFERENCE: PH-1092-PCT
; CURRENT APPLICATION NUMBER: US/10/182,018
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: JP 2000-83034
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0

```


; SEQ ID NO 75
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-018-75

Query Match 82.1%; Score 23; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 11
US-10-169-003-75
; Sequence 75, Application US/10169003
; Publication No. US20030124119A1
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical
Preparation for
; TITLE OF INVENTION: Injection
; FILE REFERENCE: PH-1093-PCT
; CURRENT APPLICATION NUMBER: US/10/169,003
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 11-375203
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-003-75

Query Match 82.1%; Score 23; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GKSIQDLRRRFFLHHLIAEIHTA 28
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKSIQDLRRRFFLHHLIAEIHTA 34

RESULT 12
US-09-843-221A-66
; Sequence 66, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN

```
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 35
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTHrP
US-09-843-221A-66
```

```
Query Match          82.1%; Score 23; DB 11; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GKSIQDLRRRFFLHHLIAEIHNTA 28
          |||||
Db      13 GKSIQDLRRRFFLHHLIAEIHNTA 35
```

RESULT 13

US-09-843-221A-64

```
; Sequence 64, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTHrP
US-09-843-221A-64
```

CC sperm DNA into a highly condensed, stable and inactive
 CC complex.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -!- MASS SPECTROMETRY: MW=3941; METHOD=Electrospray.
 DR GO; GO:0005718; C:nucleosome; NAS.
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003677; F:DNA binding activity; NAS.
 DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; NAS.
 DR GO; GO:0007076; P:mitotic chromosome condensation; NAS.
 DR GO; GO:0006334; P:nucleosome assembly; NAS.
 DR GO; GO:0007283; P:spermatogenesis; NAS.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis;
 KW DNA-binding; DNA condensation; Nuclear protein.
 FT DOMAIN 2 15 POLY-ARG.
 FT DOMAIN 17 26 POLY-ARG.
 SQ SEQUENCE 30 AA; 3943 MW; 14F1BC7E4D277049 CRC64;

 Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 13 RRR 15
 |||
 Db 2 RRR 4

RESULT 21

MMAL_DERMI

ID MMAL_DERMI STANDARD; PRT; 30 AA.
 AC P16312;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Major mite fecal allergen Der M 1 (EC 3.4.22.-) (Der M I) (Fragment).
 GN DERM1.
 OS Dermatophagoides microceras (House-dust mite).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
 OC Pyroglyphidae; Dermatophagoides.
 OX NCBI_TaxID=6955;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88229138; PubMed=3372999;
 RA Lind P., Hansen O.C., Horn N.;
 RT "The binding of mouse hybridoma and human IgE antibodies to the major
 RT fecal allergen, Der p I, of Dermatophagoides pteronyssinus. Relative
 RT binding site location and species specificity studied by solid-phase
 RT inhibition assays with radiolabeled antigen."
 RL J. Immunol. 140:4256-4262(1988).
 CC -!- FUNCTION: THIS PROTEIN IS THE MAJOR ALLERGEN OF HOUSE DUST MITE,
 CC IT IS A THIOL PROTEASE THAT HYDROLYZES PROTEINS, WITH A PREFERENCE
 CC FOR PHE OR BASIC RESIDUES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR PIR; B27634; B27634.
 DR MEROPS; C01.073; -.

DR InterPro; IPR000169; SHprot_acsite.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
 KW Hydrolase; Thiol protease; Allergen.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3314 MW; D60B742967194886 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLR 13
 |||
 Db 16 DLR 18

RESULT 22

NUO2_SOLTU

ID NUO2_SOLTU STANDARD; PRT; 30 AA.
 AC P80268;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 18 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-18KD) (CI-18KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria."
 RL Plant J. 9:357-368(1996).
 RN [2]
 RP SEQUENCE OF 1-22.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
 RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT Solanum tuberosum."
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.

KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3263 MW; 21AA88B3FAEDFE1D CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRR 14
|||
Db 24 LRR 26

RESULT 23

PRT1_CLUPA

ID PRT1_CLUPA STANDARD; PRT; 30 AA.
AC P02335;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine YII (Clupeine YII).
OS Clupea pallasii (Pacific herring), and
OS Clupea harengus (Atlantic herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
OX NCBI_TaxID=30724, 7950;
RN [1]
RP SEQUENCE.
RC SPECIES=C.pallasii;
RX MEDLINE=73223106; PubMed=4664740;
RA Suzuki K., Ando T.;
RT "Studies on protamines. XVI. The complete amino acid sequence of
RT clupeine YII.";
RL J. Biochem. 72:1419-1432(1972).
RN [2]
RP SEQUENCE.
RC SPECIES=C.harengus;
RA Chang W.J., Nukushina M., Ishii S., Nakahara C., Ando T.;
RL Submitted (AUG-1970) to the PIR data bank.
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
DR PIR; A37575; CLHR2A.
DR PIR; A38052; CLHRY2.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 30 AA; 4049 MW; 7F9BBB80F3ADA566 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
|||

Db

2 RRR 4

RESULT 24

PRT2_ONCMY

ID PRT2_ONCMY STANDARD; PRT; 30 AA.

AC P02331;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Protamine CIII (Protamine PPC 6B).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A. (CLONE CIII).

RX MEDLINE=81198983; PubMed=6262730;

RA Gedamu L., Wosnick M.A., Connor W., Watson D.C., Dixon G.H.,

RA Iatrou K.;

RT "Molecular analysis of the protamine multi-gene family in rainbow trout testis.";

RL Nucleic Acids Res. 9:1463-1482(1981).

RN [2]

RP SEQUENCE FROM N.A. (CLONE PPC 6B).

RX MEDLINE=82030654; PubMed=7287661;

RA Sakai M., Fujii-Kuriyama Y., Saito T., Muramatsu M.;

RT "Closely related mRNA sequences of protamines in rainbow trout testis.";

RL J. Biochem. 89:1863-1868(1981).

CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF

CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- TISSUE SPECIFICITY: Testis.

CC -!- MISCELLANEOUS: THE PROTAMINE CIII/PPC 6B SEQUENCE IS SHOWN.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; K03052; -; NOT_ANNOTATED_CDS.

DR PIR; A02673; IRTTC3.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

KW Testis; DNA condensation; Nuclear protein.

FT INIT_MET 0 0

FT VARIANT 10 10 V -> I (IN 18% OF THE CIII).

FT VARIANT 10 10 V -> P (IN 18% OF THE CIII).

SQ SEQUENCE 30 AA; 3991 MW; 0EBCBF9DC788EFA7 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
|||
Db 2 RRR 4

RESULT 25

PRT3_ONCMY

ID PRT3_ONCMY STANDARD; PRT; 30 AA.

AC P02332;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last annotation update)

DE Protamine 1B.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A. (CLONES PRTP178 AND PRTP94).

RX MEDLINE=81198983; PubMed=6262730;

RA Gedamu L., Wosnick M.A., Connor W., Watson D.C., Dixon G.H.,

RA Iatrou K.;

RT "Molecular analysis of the protamine multi-gene family in rainbow

RT trout testis.";

RL Nucleic Acids Res. 9:1463-1482(1981).

RN [2]

RP SEQUENCE.

RX MEDLINE=86274711; PubMed=3755398;

RA McKay D.J., Renaux B.S., Dixon G.H.;

RT "Rainbow trout protamines. Amino acid sequences of six distinct

RT proteins from a single testis.";

RL Eur. J. Biochem. 158:361-366(1986).

CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF

CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- TISSUE SPECIFICITY: Testis.

CC -!- MISCELLANEOUS: BOTH OF THESE SEQUENCES DIFFER FROM ONE OF THE

CC PROTAMINE CIII MINOR COMPONENTS IN HAVING 9-ARG INSTEAD OF 9-PRO.

DR PIR; A93723; ITR78.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

KW Testis; DNA condensation; Nuclear protein.

FT INIT_MET 0 0

SQ SEQUENCE 30 AA; 4064 MW; 0EBCBF9DD1E78947 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
|||
Db 2 RRR 4

RESULT 26

PRT4_ONCMY

ID PRT4_ONCMY STANDARD; PRT; 30 AA.
 AC P02333;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Protamine PTP4.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=79199790; PubMed=450133;
 RA Jenkins J.R.;
 RT "Sequence divergence of rainbow trout protamine mRNAs; comparison of
 RT coding and non-coding nucleotide sequences in three protamine cDNA
 RT plasmids.";
 RL Nature 279:809-811(1979).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -----
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 CC -----
 DR EMBL; X01204; CAA25623.1; -.
 DR PIR; A02675; ITR4.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 FT INIT_MET 0 0
 SQ SEQUENCE 30 AA; 4064 MW; 0EBCBF9DCD979537 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RRR 15
 |||
 Db 2 RRR 4

RESULT 27

PRTB_ONCMY

ID PRTB_ONCMY STANDARD; PRT; 30 AA.
 AC P12819;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protamine 1A (Protamine PRTP43/PPC 2E).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86274711; PubMed=3755398;
 RA McKay D.J., Renaux B.S., Dixon G.H.;
 RT "Rainbow trout protamines. Amino acid sequences of six distinct
 RT proteins from a single testis.";
 RL Eur. J. Biochem. 158:361-366(1986).
 RN [2]
 RP SEQUENCE FROM N.A. (CLONE PRTP43).
 RX MEDLINE=81198983; PubMed=6262730;
 RA Gedamu L., Wosnick M.A., Connor W., Watson D.C., Dixon G.H.,
 RA Iatrou K.;
 RT "Molecular analysis of the protamine multi-gene family in rainbow
 RT trout testis.";
 RL Nucleic Acids Res. 9:1463-1482(1981).
 RN [3]
 RP SEQUENCE FROM N.A. (CLONE PPC 2E).
 RX MEDLINE=82030654; PubMed=7287661;
 RA Sakai M., Fujii-Kuriyama Y., Saito T., Muramatsu M.;
 RT "Closely related mRNA sequences of protamines in rainbow trout
 RT testis.";
 RL J. Biochem. 89:1863-1868(1981).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -----
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 CC -----
 DR EMBL; K03052; AAA49607.1; -.
 DR EMBL; K03051; AAA49606.1; -.
 DR PIR; B02673; IRTRC2.
 DR PIR; I51349; I51349.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 FT INIT_MET 0 0
 SQ SEQUENCE 30 AA; 4050 MW; 0EBCBF9DC78B5947 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

|||
2 RRR 4

RESULT 28

PSAM_ODOSI

ID PSAM_ODOSI STANDARD; PRT; 30 AA.
AC P49487;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Photosystem I reaction centre subunit XII (PSI-M).
GN PSAM.
OS Odontella sinensis (Marine centric diatom).
OG Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
OX NCBI_TaxID=2839;
RN [1]
RP SEQUENCE FROM N.A.
RA Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis.";
RL Plant Mol. Biol. Rep. 13:336-342(1995).
CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
CC -----
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CC -----
DR EMBL; Z67753; CAA91676.1; -.
DR PIR; S78303; S78303.
KW Photosystem I; Photosynthesis; Chloroplast.
SQ SEQUENCE 30 AA; 3329 MW; 73FDEB91E4BF634F CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LIA 23
|||
Db 12 LIA 14

RESULT 29

PSAM_PINTH

ID PSAM_PINTH STANDARD; PRT; 30 AA.
AC P41601;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Photosystem I reaction centre subunit XII (PSI-M).
GN PSAM.

OS *Pinus thunbergii* (Green pine) (Japanese black pine).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95024047; PubMed=7937893;
 RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
 RA Sugiura M.;
 RT "Loss of all ndh genes as determined by sequencing the entire
 RT chloroplast genome of the black pine *Pinus thunbergii*."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
 CC -----
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 CC -----
 DR EMBL; D17510; BAA04383.1; -.
 DR EMBL; D17510; BAA04316.1; -.
 DR PIR; T07505; T07505.
 KW Photosystem I; Photosynthesis; Chloroplast.
 SQ SEQUENCE 30 AA; 3321 MW; A150441AB5D5AF7C CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 LIA 23
 |||
 Db 7 LIA 9

RESULT 30
 PSAM_PORPU
 ID PSAM_PORPU STANDARD; PRT; 30 AA.
 AC P51395;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Photosystem I reaction centre subunit XII (PSI-M).
 GN PSAM.
 OS *Porphyra purpurea*.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TaxID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RA Reith M.E., Munholland J.;
 RT "Complete nucleotide sequence of the *Porphyra purpurea* chloroplast
 RT genome.";

RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
 CC -----
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 CC -----
 DR EMBL; U38804; AAC08281.1; -.
 DR PIR; S73316; S73316.
 KW Photosystem I; Photosynthesis; Chloroplast.
 SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LGK 7
 |||
 Db 24 LGK 26

RESULT 31

RL18_HALCU
 ID RL18_HALCU STANDARD; PRT; 30 AA.
 AC P05970;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S ribosomal protein L18P (HCUL18) (HL13) (Fragment).
 GN RPL18P.
 OS Halobacterium cutirubrum.
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=2242;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79045279; PubMed=152199;
 RA Smith N., Matheson A.T., Yaguchi M., Willick G., Nazar R.N.;
 RT "The 5-S RNA-protein complex from an extreme halophile,
 RT Halobacterium cutirubrum. Purification and characterization."
 RL Eur. J. Biochem. 89:501-509(1978).
 CC -!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
 DR PIR; S07217; S07217.
 KW Ribosomal protein.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3624 MW; 3A50079B1569CB74 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
 |||

Db 11 RRR 13

RESULT 32

COX4_NEUCR

ID COX4_NEUCR STANDARD; PRT; 31 AA.
AC P06809;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome c oxidase polypeptide IV, mitochondrial precursor
DE (EC 1.9.3.1) (Fragment).
GN COX-4.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86085927; PubMed=3001085;
RA Sachs M.S., David M., Werner S., Rajbhandary U.L.;
RT "Nuclear genes for cytochrome c oxidase subunits of Neurospora
RT crassa. Isolation and characterization of cDNA clones for subunits
RT IV, V, VI, and possibly VII.";
RL J. Biol. Chem. 261:869-873(1986).
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
CC -----
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CC -----
DR EMBL; M12116; AAA33574.1; -.
DR PIR; A25629; A25629.
KW Oxidoreductase; Mitochondrion; Inner membrane; Transit peptide.
FT NON_TER 1 1
FT TRANSIT <1 16 MITOCHONDRION.
FT CHAIN 17 >31 CYTOCHROME C OXIDASE POLYPEPTIDE IV.
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3397 MW; 069F5D5510300362 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRR 14
|||
Db 5 LRR 7

RESULT 33

DEJP_DROME

ID DEJP_DROME STANDARD; PRT; 31 AA.
AC P81160;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ductus ejaculatorius peptide 99B.
GN DUP99B.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE OF 1-24 FROM N.A., AND SEQUENCE OF 9-31.
RC STRAIN=Oregon-R; TISSUE=Ductus ejaculatorius;
RX MEDLINE=21835775; PubMed=11846801;
RA Saudan P., Hauck K., Soller M., Choffat Y., Ottiger M., Sporri M.,
RA Ding Z., Hess D., Gehrig P.M., Klauser S., Hunziker P., Kubli E.;
RT "Ductus ejaculatorius peptide 99B (DUP99B), a novel Drosophila
RT melanogaster sex-peptide pheromone.";
RL Eur. J. Biochem. 269:989-997(2002).
CC -!- FUNCTION: INDUCES POST-MATING RESPONSES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: DUCTUS EJACULATORIUS.
CC -!- SIMILARITY: TO PARAGONIAL PEPTIDE B.
DR FlyBase; FBgn0024381; Dup99B.
DR GO; GO:0045434; P:negative regulation of female receptivity, . . .; IMP.
DR GO; GO:0046662; P:regulation of oviposition; NAS.
KW Behavior; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 19 31
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 31 AA; 3766 MW; B90A9B99C120EF49 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NLG 6
|||
Db 22 NLG 24

RESULT 34

GP37_BPSP1

ID GP37_BPSP1 STANDARD; PRT; 31 AA.
AC O48393;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Putative gene 37 protein.
GN 37.
OS Bacteriophage SP01.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC SP01-like viruses.
OX NCBI_TaxID=10685;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98327781; PubMed=9657951;
 RA Stewart C.R., Gaslightwala I., Hinata K., Krolikowski K.A.,
 RA Needleman D.S., Peng A.S.-Y., Peterman M.A., Tobias A., Wei P.;
 RT "Genes and regulatory sites of the 'host-takeover module' in the
 RT terminal redundancy of Bacillus subtilis bacteriophage SPO1.";
 RL Virology 246:329-340(1998).
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 CC -----
 DR EMBL; AF031901; AAC29006.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 31 AA; 3715 MW; 5ECBA628AF320670 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
 |||
 Db 29 RRR 31

RESULT 35

NAP4_HUMAN

ID NAP4_HUMAN STANDARD; PRT; 31 AA.
 AC P19877;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neutrophil-activating protein 4 (NAP-4) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Platelet;
 RX MEDLINE=91054515; PubMed=2241978;
 RA Schroeder J.-M., Sticherling M., Persoon N.L.M., Christophers E.;
 RT "Identification of a novel platelet-derived neutrophil-chemotactic
 RT polypeptide with structural homology to platelet-factor 4.";
 RL Biochem. Biophys. Res. Commun. 172:898-904(1990).
 CC -!- FUNCTION: INDUCES CHEMOTAXIS OF NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC). BUT LACK THE C-X-C OR C-C MOTIFS.
 DR PIR; A36162; A36162.
 DR HSSP; P02776; 1RHP.
 DR GO; GO:0008009; F:chemokine activity; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.

DR InterPro; IPR000827; CC_chemkine_sml.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; PARTIAL.
 KW Chemotaxis; Growth factor.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3447 MW; AD910FB894EC1760 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QDL 12
 |||
 Db 6 QDL 8

RESULT 36

PETL_ODOSI

ID PETL_ODOSI STANDARD; PRT; 31 AA.
 AC P49524;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit
 DE petL).
 GN PETL.
 OS Odontella sinensis (Marine centric diatom).
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
 OX NCBI_TaxID=2839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
 RT "The chloroplast genome of a chlorophyll a+c-containing alga,
 RT Odontella sinensis.";
 RL Plant Mol. Biol. Rep. 13:336-342(1995).
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated.
 CC -!- SIMILARITY: Belongs to the petL family.
 CC -----
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 CC -----
 DR EMBL; Z67753; CAA91708.1; -.
 DR PIR; S78335; S78335.
 DR HAMAP; MF_00433; -; 1.
 DR Pfam; PF05115; PetL; 1.
 KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;

KW Thylakoid.
FT TRANSMEM 4 24 POTENTIAL.
SQ SEQUENCE 31 AA; 3459 MW; AD65232A8B27853E CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KSI 9
|||
Db 26 KSI 28

RESULT 37

PRT2_CLUPA

ID PRT2_CLUPA STANDARD; PRT; 31 AA.
AC P02336;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine Z (Clupeine Z).
OS Clupea pallasii (Pacific herring), and
OS Clupea harengus (Atlantic herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
OX NCBI_TaxID=30724, 7950;
RN [1]
RP SEQUENCE.
RC SPECIES=C.pallasii;
RX MEDLINE=71157437; PubMed=5551645;
RA Iwai K., Nakahara C., Ando T.;
RT "Studies on protamines. XV. The complete amino acid sequence of the Z
RT component of clupeine. Application of N leads to O acyl rearrangement
RT and selective hydrolysis in sequence determination.";
RL J. Biochem. 69:493-509(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=C.harengus;
RA Chang W.J., Nukushina M., Ishii S., Nakahara C., Ando T.;
RL Submitted (AUG-1970) to the PIR data bank.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92126280; PubMed=1772633;
RA Balschmidt P., Hansen F.B., Dodson E., Dodson G., Korber F.;
RT "Structure of porcine insulin cocrystallized with clupeine Z.";
RL Acta Crystallogr. B 47:975-986(1991).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- MISCELLANEOUS: CLUPEINE Z IS PROBABLY THE RESULT OF A CROSSOVER
CC BETWEEN THE GENES FOR CLUPEINES YI AND YII.
DR PIR; A37576; CLHRZA.
DR PIR; A38053; CLHRZ.
DR PDB; 7INS; 31-JAN-94.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein; 3D-structure.
SQ SEQUENCE 31 AA; 4165 MW; 092CCBF7F3AFC050 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
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Db 2 RRR 4

RESULT 38

PRT3_CLUPA

ID PRT3_CLUPA STANDARD; PRT; 31 AA.
AC P02337;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine YI (Clupeine YI).
OS Clupea pallasii (Pacific herring), and
OS Clupea harengus (Atlantic herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
OX NCBI_TaxID=30724, 7950;
RN [1]
RP SEQUENCE.
RC SPECIES=C.pallasii;
RX MEDLINE=73223107; PubMed=4664741;
RA Suzuki K., Ando T.;
RT "Studies on protamines. XVII. The complete amino acid sequence of
RT clupeine YI.";
RL J. Biochem. 72:1433-1446(1972).
RN [2]
RP SEQUENCE.
RC SPECIES=C.harengus;
RA Chang W.J., Nukushina M., Ishii S., Nakahara C., Ando T.;
RL Submitted (AUG-1970) to the PIR data bank.
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
DR PIR; A37577; CLHR1A.
DR PIR; A38051; CLHRY1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 31 AA; 4112 MW; BDCC9A140FF7F819 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RRR 15
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RESULT 39

SCK5_ANDMA

ID SCK5_ANDMA STANDARD; PRT; 31 AA.
AC P31719;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leiurotoxin I-like toxin P05.
OS Androctonus mauretanicus mauretanicus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Androctonus.
OX NCBI_TaxID=6860;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93215831; PubMed=8385026;
RA Zerrouk H., Mansuelle P., Benslimane A., Rochat H.,
RA Martin-Eauclaire M.-F.;
RT "Characterization of a new leiurotoxin I-like scorpion toxin. P05
RT from Androctonus mauretanicus mauretanicus.";
RL FEBS Lett. 320:189-192(1993).
RN [2]
RP SYNTHESIS.
RX MEDLINE=93208090; PubMed=8457543;
RA Sabatier J.-M., Zerrouk H., Darbon H., Mabrouk K., Benslimane A.,
RA Rochat H., Martin-Eauclaire M.-F., van Rietschoten J.;
RT "P05, a new leiurotoxin I-like scorpion toxin: synthesis and
RT structure-activity relationships of the alpha-amidated analog, a
RT ligand of Ca(2+)-activated K⁺ channels with increased affinity.";
RL Biochemistry 32:2763-2770(1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=94032328; PubMed=8218272;
RA Meunier S., Bernassau J.-M., Sabatier J.-M., Martin-Eauclaire M.-F.,
RA van Rietschoten J., Cambillau C., Darbon H.;
RT "Solution structure of P05-NH2, a scorpion toxin analog with high
RT affinity for the apamin-sensitive potassium channel.";
RL Biochemistry 32:11969-11976(1993).
CC -!- FUNCTION: Blocker for the small conductance calcium-activated
CC potassium channels (SK-Ca) (also known as apamine-sensitive
CC potassium channel).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC CHANNEL INHIBITORS SUBFAMILY.
DR PIR; A49078; A49078.
DR PDB; 1PNH; 31-JAN-94.
DR InterPro; IPR001947; Scorpion_toxinS.
DR Pfam; PF00451; toxin_2; 1.
DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor; 3D-structure.
FT DISULFID 3 21
FT DISULFID 8 26

FT DISULFID 12 28
 FT HELIX 5 13
 FT TURN 14 15
 FT STRAND 18 22
 FT TURN 23 24
 FT STRAND 25 29
 SQ SEQUENCE 31 AA; 3421 MW; 94B06CDC5CFB46FE CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LRR 14
 |||
 Db 5 LRR 7

RESULT 40

SCKL_LEIQH

ID SCKL_LEIQH STANDARD; PRT; 31 AA.

AC P16341;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leiurotoxin I (LeTx I) (Scyllatoxin).

OS Leiurus quinquestriatus hebraeus (Yellow scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Buthoidea; Buthidae; Leiurus.

OX NCBI_TaxID=6884;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=88273110; PubMed=2839478;

RA Chicci G.G., Gimenez-Gallego G., Ber E., Garcia M.L., Winkquist R.,

RA Cascieri M.A.;

RT "Purification and characterization of a unique, potent inhibitor of

RT apamin binding from Leiurus quinquestriatus hebraeus venom.";

RL J. Biol. Chem. 263:10192-10197(1988).

RN [2]

RP SYNTHESIS.

RX MEDLINE=90170992; PubMed=2307683;

RA Auguste P., Hugues M., Grave B., Gesquiere J.C., Maes P., Tartar A.,

RA Romey G., Schweitz H., Lazdunski M.;

RT "Leiurotoxin I (scyllatoxin), a peptide ligand for Ca2(+)-activated

RT K+ channels. Chemical synthesis, radiolabeling, and receptor

RT characterization.";

RL J. Biol. Chem. 265:4753-4759(1990).

RN [3]

RP STRUCTURE BY NMR.

RX MEDLINE=90127439; PubMed=2153586;

RA Martins J.C., Zhang W., Tartar A., Lazdunski M., Borremans F.A.M.;

RT "Solution conformation of leiurotoxin I (scyllatoxin) by 1H nuclear

RT magnetic resonance. Resonance assignment and secondary structure.";

RL FEBS Lett. 260:249-253(1990).

CC -!- FUNCTION: Blocker for the small conductance calcium-activated

CC potassium channels (SK-Ca) (also known as apamine-sensitive

CC potassium channel).

```

CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC  -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC      CHANNEL INHIBITORS SUBFAMILY.
DR  PIR; A28805; A28805.
DR  PDB; 1SCY; 26-JAN-95.
DR  InterPro; IPR001947; Scorpion_toxins.
DR  Pfam; PF00451; toxin_2; 1.
DR  PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW  Toxin; Neurotoxin; Ionic channel inhibitor;
KW  Potassium channel inhibitor; Amidation; 3D-structure.
FT  DISULFID      3      21
FT  DISULFID      8      26
FT  DISULFID     12      28
FT  MOD_RES      31      31      AMIDATION.
FT  HELIX         5      14
FT  TURN         15      16
FT  STRAND       18      21
FT  STRAND       26      29
SQ  SEQUENCE     31 AA;  3430 MW;  BB3183DC5CEA53A7 CRC64;

Query Match          10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy          5 LGK 7
           |||
Db          18 LGK 20

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